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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 2, 2002, 12:15:08; Search time 17.4 Seconds (without alignments) 745.463 Million cell updates/sec Run on:

US-09-810-506-2 1816 1 MAPEINTKLTVPVHSATGGE......FIEALSEAGALQYVKAPSAA 335 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		d			SUMMAKIES	
Result		Query				
No.	Score	Match	Length	DB	QI	Description
1	243	13.4	332		GLYG_MOUSE	mus m
7	241	13.3	349	Н	GLYG_HUMAN	homo
٣	240	13.2	501	Н	GYG2_HUMAN	homo
4	235.5	13.0	332	٦	GLYG_RABIT	oryct
S	231	12.7	332	_	GLYG_RAT	
9	165	9.1	371	Н	YA0C_SCHPO	Q09680 schizosacch
7	129.5	7.1	380	Н	GLG2_YEAST	
œ	122	6.7	618	Н	GLG1_YEAST	
σ	110	6.1	286	Н	GSPA_BACSU	
10	105	5.8	1251	Н	YMI1_YEAST	Q04545 saccharomyc
11	103.5	5.7	2157	Н	POLG_HRV1B	P12916 human rhino
12	96.5	5.3	338	7	RFAJ_ECOLI	_
13	94.5	5.2	443	٦	COBB_METJA	_
14	93.5	5.1	337	.	RFAI_SALTY	
15	93.5	5.1	623	Н	HCYE_EURCA	P02242 eurypelma c
16	66	5.1	862	Н	LOXA_PHAVU	
17	92	5.1	630	Н	TNPE_STAAU	
18	92	5.1	2151	Н	RRPL_HANTV	
19	91.5	5.0	336	Т	RFAJ_SALTY	
20	91.5	5.0	342	1	SPDE_LYCES	Q9zs45 lycopersico
21	91	2.0	315	Н	SPD1_HYONI	
22	90	5.0	372	~	GMDS_HUMAN	
23	89.5	4.9	759	Н	ARY2_CALVI	
24	æ	4.8	824	Н	TGLK_RAT	P23606 rattus norv
25	87.5	4.8	324	Н	CP21_HORVU	P55747 hordeum vul
26	87	4.8	285	Н	Y714_STRCO	0
27	87	4.8	166	Н	DPP4_HUMAN	
28	86.5	4.8	570	7	NCAP_MOPEI	<u>о</u>
29	98	4.7	314	Н	SPDE_NICSY	048660 nicotiana s
30	\sim	4.7	317	-		_
31	85.5	4.7	450	Н	VD10_BPT5	7
32		4.7	630	Н	TNPB_STAAU	
33		4.7	697	Н	YHF0_YEAST	P38721 saccharomyc

P29044 barley yell P04958 clostridium	P22735 homo sapien P04821 saccharomyc	Q58617 methanococc	P19573 pseudomonas	P13186 saccharomyc	P38444 rattus norv	P27209 tobacco nec	P09505 barley yell	Q9plc6 chlamydia m	P06961 escherichia
RRPO_BYDV1 TETX_CLOTE	TGLK_HUMAN CC25_YEAST	YC20_METJA	NOSZ_PSEST	KIN2_YEAST	AVR2_RAT	RRPO_TNVD	RRPO_BYDVP	SYG_CHLMU	CCA_ECOLI
ч -		П	Н		٦	7	7	П	1
867 1314	817 1589	578	638	1147	513	724	867	1003	412
4.7	4.7	4.7	4.7	4.7	4.6	4.6	4.6	4.6	4.6
85.5 85.5	85 85	84.5	84.5	84.5	83.5	83.5	83.5	83.5	83
34 35	36 37	38	36	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 GLYG_MOUSE STANDARD; PRT; 332 AA. ID GLYG_MOUSE STANDARD;

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22 RAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQL--VDQGCVVKE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 24.8% hes 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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                                                                 GYG2
                                                                                     [9]
  δλ
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                                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The human intron-containing gene for glycogenin maps to chromosome 3,
                                                                                                                    80 IEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDLPNGQF 139
                                                                                                                               62 VLDSGDSAHLTLMKRPELGITLTKLHCWSLTQYSKCVFMDADTLVLSNIDDLFEREE--- 118
                                                                                                                                                            140 YAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYH 199
                                                                                                                                                                                 119 ------FNSGVFVYQPSIETYN 146
                                                                                                                                                                                                       252
                                                                                                                                                                                                                  253 VKVVHYCAAGAKPWRFTGEEE----NMDREDIKM----LVKKWWDIYNDE---SLDYKNV 301
                                                                                                                                                                                                                                                                    207 AKVVHFLGR-TKPWNYTYNPQTKSVNCDSQDPTVSHPEFLNLWWDTFTTNVLPLLQHHGL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ď
                                                     64; Gaps
                                                                        22 RAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQL--VDQGCVVKE 79
                                                                                       3 QAFVT-LTTNDAYAKGALVLGSSLKQHRTTRRMVVLTSPQVSDSMRKVLETVFDDVIMVD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM GN-1).
TISSEDS-Exheletal muscle;
MEDIATNE-96176958; PubMed-8602861;
Barbetti F., Rocchi M., Bossolasco M., Cordera R., Sbraccia P.,
Finelli P., Consalez G.G.;
"The human skeletal muscle glycogenin gene: cDNA, tissue expression and chromosomal localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   οĘ
                                                                                                                                                                                                     200 NLLETVKIVPPILFAEQDFLNMYFK-----DIYKPIPPVYNLVLAMLWRHPENIEL--DQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99326495; PubMed-10395894; Van Maanen M.H., Fournier P.N., Palmer T.N., Abraham L.J.; Characterization of the human glycogenin-1 gene: identification muscle-specific regulatory domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lomako J., Mazuruk K., Lomako W.M., Alonso M.D., Whelan W.J., Rodriguez I.R.;
                                Length 332;
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leffers H., Wiemann S., Ansorge W.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
37271 MW; 8DA0F1A875552F40 CRC64;
                               and chromosomal localization.";
Blochem. Blophys. Res. Commun. 220:72-77(1996).
                                                                                                                                                                                                                                                                                                                                                                266 V-----KDASSYLMMEHVSGALSDLSFGEAPAA 293
                                                                                                                                                                                                                                                                                         302 VIGDSHKKQQTLQQFIEALSEA-GALQYVKAPSA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM GN-1S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM GN-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM GN-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96299648; PubMed=8661012
                              Query Match
Best Local Similarity 25.1%;
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               band q24.";
Genomics 33:519-522(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Skin;
SEQUENCE
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                                                          SEQUENCE FROM N.A. (ISOFORM GN-1L), AND ALTERNATIVE SPLICING. MEDLINE-20184/41, PubMed=10721716; Zhai L., Mu J., Zong H., DePsoli-exach A.A., Roach P.J.; Rutali L., Mu dnd chromosomal localization of the human glycogenin-2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- COFACTOR: SELP-GLUCOSYLATION IS DEPENDENT ON THE PRESENCE OF DIVALENT METAL IONS OF WHICH MANGANESE ION IS THE MOST EFFECTIVE.
-!- PATHWAY: GLYCOGEN BIOSYNTHESIS.
-!- SUBUNIT: HOMODIMER, TIGHTLY COMPLEXED TO GLYCOGEN SYNTHASE.
-!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; GN-1L (SHOWN HERE), GN-1 AND GN-1S, ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- PTM: SELF-GLYCOSYLATED BY THE TRANSFER OF GLUCOSE RESIDUES FROM UDP-GLUCOSE TO ITSELF, FORMING AN ALPHA-1,4-GLYCOA OF AROUND 10
                                                                                                                                                                                                                                                                                                                                                                                                                               5
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O-LINKED (GLC. ) (BY SIMILARITY).
MISSING (IN ISOFORM GN-1S).

CAIBCCFF54C8AF09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; 19R002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
Transferase; Glycogen biosynthesis; Acetylation; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: SELF-GLUCOSYLATES, VIA AN INTER-SUBUNIT MECHANISM, FORM AN OLIGOSACCHARIDE PRIMER THAT SERVES AS SUBSTRATE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESIDUES ATTACHED TO TYR-194.
-!- SIMILARITY: BELONGS TO THE GLYCOGENIN FAMILY.
-!- CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.3%; Score 241; DB 1; Length 349; 24.8%; Pred. No. 1.4e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X79537; CAA56073.1; ALT_FRAME.
EMBL; AF065481; AAD31084.1; '-
EMBL; AF065476; AAD31084.1; JOINED.
EMBL; AF065477; AAD31084.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF065478; AAD31084.1; JOINED.
EMBL; AF065479; AAD31084.1; JOINED.
EMBL; AF065480; AAD31084.1; JOINED.
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM GN-1).
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Gene 234:217-226(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glucosylglycogenin.
                                                                                                                                                                                                                               Gene 242:229-235(2000)
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292
292
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                                                                                                                                                                                                                                                                                                                               TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 603942;
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Indels 74; Gaps

43; Mismatches 120;

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zhai L., Mu J., Zong H., DePaoli-Roach A.A., Roach P.J.;
"Structure and chromosomal localization of the human glycogenin-2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIVALENT METAL IONS OF WHICH MANGANESE ION IS THE MOST EFFECTIVE.
--- PATHARY: GLYCOGEN BIOSYNTHESIS.
--- SUBUNIT: HOMODIMER, TIGHTLY COMPLEXED TO GLYCOGEN SYNTHASE.
--- ALTERNATIVE PRODUCTS: AT LEAST 6 ISOFORMS; ALPHA (SHOWN HERE),
BETA, GAMMA, DELIA, EPSILON AND ZETA; ARE PRODUCED BY ALTERNATIVE
IEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDLPNGQF 139
                    140 YAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYH 199
                                                                                                    -------LSAAPDP-GWPDC-----FNSGVFVYQPSVETYN 146
                                                                                                                                          200 NLLETVKIVPPTLFAEQDFLNMYFK-----DIYKPIPPVYNLVLAMLWRHPENIEL--DQ 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mu J., Skurat A.V., Roach P.J.;
"Glycogenin-2, a novel self-glucosylating protein involved in liver glycogen biosynthesis."
J. Biol. Chem. 272:27589-27597(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryoia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                               253 VKVVHYCAAGAKPWRFT------GEEENMDREDIKMLVKKWWDIYNDESLDYKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mu J., Roach P.J.;
"Characterization of human glycogenin-2, a self-glucosylating initiator of liver glycogen metabolism.";
J. Biol. Chem. 273:34850-34856(1989)
- FUNCTION: SELF-GLUCOSYLAFES, VIA AN INTER-SUBUNIT MECHANISM, FORM AN OLIGOSACCHARIDE PRIMER THAT SERVES AS SUBSTRATE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glucosylglycogenin. COFACTOR: SELF-GLUCOSYLATION IS DEPENDENT ON THE PRESENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: UDP-glucose + glycogenin = UDP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION, AND CARBOHYDRATE-LINKAGE SITE TYR-228
MEDLINE-99074257; PubMed-9857012;
                                                                                                                                                                                                                                                                                                                                                                                                          GYG2_HUMAN STANDARD; PRT; 501 AA. 015488; 015489; 015489; 015490; 015486; 015485; 015487; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) GLYcogenin-2 (EC 2.4.1.186) (GN-2) (GN2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=20184741; Pubmed=10721716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98010589; PubMed=9346895;
                                                                                                                                                                                                                                                                                    302 VIGDSHKKQQTLQQF 316
                                                                                                                                                                                                                                                                                                                      ------PLLQQF 263
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TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN LIVER, HEART, AND

PTM: SELF-GLYCOSYLATED BY THE TRANSFER OF GLUCOSE RESIDUES FROM UDP-GLUCOSE TO ITSELF, FORMING AN ALPHA-1,4-GLYCAN OF AROUND 10

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 TYHNLLETVKIVPPTLFAEQDFLNMYFK-----DIYKPIPPVYNLVLAMLWRHPENIEL- 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 - DQVKVVHYCAAGAKPWRFTGEEEN----MDREDIK------MLVKKWWDIYNDESLD-YK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 GSSAKVVHFLGS-MKPWNYKYNPQSGSVLEQGSVSSSQHQAAFLHLWWTVYQNNVLPLYK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 PVYPPENQTEFAMAYYV----INYSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDLPN 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 EVNLIDSADYIHLAFLKRPELGLTLTKLHCWTLTHYSKCVFLDADTLVLSNVDELFD--R 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 GEFSAAPD-----FNSGVFVFQPSLH 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 RAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKEIE 81
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EKV -> AGI (IN REF. 1; AAB84376)
2EDE05FDAD5A7657 CRC64;
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MISSING (IN ISOFORM BETA).
MISSING (IN ISOFORM GAMMA).
MISSING (IN ISOFORM DELTA).
MISSING (IN ISOFORM EPSILON).
MISSING (IN ISOFORM ZETA).
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Pfam; PF01501; Glyco_transf_8; 1.
Transferase; Glycogen biosynthesis; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y->F: LOSS OF ACTIVITY.
Y->F: NO LOSS OF ACTIVITY.
             SIMILARITY: BELONGS TO THE GLYCOGENIN FAMILY.
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/FTId=VAR_010401.
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                                                                                                                                                                                                                                                                                                                              AF179617; AAF61855.1; JOINED.
AF179618; AAF61855.1; JOINED.
AF179619; AAF61855.1; JOINED.
AF179620; AAF61855.1; JOINED.
AF179621; AAF61855.1; JOINED.
                                                                                                                                                                                                                                                                                 AF179624; AAF61855.1; AR179615; AAF61855.1; JOINED AF179616; AAF61855.1; JOINED.
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RESIDUES ATTACHED TO TYR-228
                                                                                                                                                                    EMBL; U94362; AAB84377.1; --
EMBL; U94364; AAB84378.1; --
EMBL; U94457; AAB84373.1; --
EMBL; U94357; AAB84373.1; --
EMBL; U94360; AAB84374.1; --
EMBL; U94360; AAB84376.1; --
EMBL; U94361; AAB84376.1; --
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462
501 AA;
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Matches 78; Conserv
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ACT_SITE 111
CARBOHYD 22
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"The amino acid sequence of rabbit skeletal muscle glycogenin.";
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-!- FUNCTION: SELF-GLUCOSYLATES, VIA AN INTER-SUBUNIT MECHANISM,
FORM AN OLIGOSACCHARIDE PRIMER THAT SERVES AS SUBSTRATE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lomako J., Whelan W.J.;
"The occurrence of serine phosphate in glycogenin: a possible
                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93100288; PubMed-1281472;
Viskupic E., Cao Y., Zhang W., Cheng C., Depaoli-Roach A.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLYCOGEN SYNTHASE.
CATALYTIC ACTIVITY: UDP-glucose + glycogenin = UDP +
glucosylglycogenin.
                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eui
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-NEW ZEALAND WHITE; TISSUE-Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 34-47; 181-201; 209-226 AND 307-324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION.
MEDLINE-92289736; PubMed=7771798;
MEDLINE-92289736; PubMed=7771798;
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                                                                                                                                                      01-JAN-1990 (Rel. 13, Created)
01-007-1993 (Rel. 27, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
61ycogenin-1 (EC 2.4.1.186).
                                                                                                                       332 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 34-47, AND PHOSPHORYLATION.
MEDLINE-89374676; Pubmed-3151442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90032666; PubMed-2806254;
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MEDLINE-94192798; PubMed-8143846;
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                                                                                                                                                                                                                                            Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulatory site.";
Biofactors 1:261-264(1988).
                                                                                                                       STANDARD;
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300 NVVIGDS 306
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297 SVQAGEA 303
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                                                                                                                                                                                                                              GYG OR GYG1.
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                                                                                                                      GLYG_RABIT
P13280;
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                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 YAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYH 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COFACTOR: SELF-GLUCOSYLATION IS DEPENDENT ON THE PRESENCE OF DIVALENT METAL IONS OF WHICH MANGANESE ION IS THE MOST EFFECTIVE. PATHWAY: GLYCOGEN BIOSYNTHESIS.
SUBUNIT: HOMODIMER TIGHTLY COMPLEXED TO THE 86 KDA CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 AKVVHFLGQ-TKPWNYTYDTKTKSVRSEGHDPTMTH---PQFLNVWWDIFTTSVVPLLQQ 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                              SUBUNIT OF GLYCOGEN SYNTHASE.
PTM: SELF-GLYCOSYLATED BY THE TRANSFER OF GLUCOSE RESIDUES FROM UDP-GLUCOSE TO ITSELF. FORMING AN ALPHA-1,4-GLYCAN OF AROUND 10 RESIDUES ATTACHED TO TYR-194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 FGLVQDTCSYQHVEDVSGAVSHLSLGETPATTQPFVSSEERKERWEGGQADYMGADS 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 ----DESLDYKNV--VIGD-SH----KKQQTLQQFIEALS-----EAGALQYVKAPS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 NLLETVKIVPPTLFAEQDFLNMYFK-----DIYKPIPPVYNLVLAMLWRHPENIEL--DQ
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Transferase; Glycogen biosynthesis; Acetylation; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.0%; Score 235.5; DB 1; Length 332; 23.8%; Pred. No. 4.1e-13;
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                                                                                                                                SIMILARITY: BELONGS TO THE GLYCOGENIN FAMILY.
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Last annotation update)
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PIR; A45094; A45094.
InterPro; IPR002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
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INIT_MET
ACT_SITE
MOD_RES
MOD_RES
CARBOHYD 19
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CONFLICT
SEQUENCE
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GLG2 OR YJL137C OR J0663.
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Q09680:
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P47011;
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GLG2_YEAST
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 YAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYH 199
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                                                                                                                  STRAIN-WISTAR; TISSUE-Heart; Pang S.C.; Pang S.C.; Molecular cloning and developmental expression of rat glycogenin in
                                                                                                                                                                                                                                                                     COFACTOR: SELF-GLUCOSYLATION IS DEPENDENT ON THE PRESENCE OF DIVALENT METAL IONS OF WHICH MANGANESE ION IS THE MOST EFFECTIVE
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                                                                                                                                                                                                                                                                                                               PATHWAY: GLYCOĞEN BIOSYNTHESIS.
SUBUNTT: HOMODINER TIGHTLY COMPLEXED TO THE 86 KDA CATALYTIC
SUBUNTT: HOMODINER TIGHTLY COMPLEXED TO THE 86 KDA CATALYTIC
SUBUNTT OF GLYCOĞEN SYNTHASE (BY SIMILARITY).

PTM: SELF-GLYCOĞYLATED BY THE TRANSFER OF GLUCOSE RESIDUES FROM
UDP-GLUCOSE TO ITSELF, FORNING NA ALPHA-1, 4-GLYCAN OF AROUND 10
RESIDUES ATTACHED TO TYR-194 (BY SIMILARITY).
SIMILARITY: BELONGS TO THE GLYCOĞENIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: SELF-GLUCOSYLATES, VIA AN INTER-SUBUNIT MECHANISM, FORM AN OLIGOSACCHARIDE PINMER THAT SERVES AS SUBSTRATE FOR GLYCOGEN SYNTHARE (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: UDP-glucose + glycogenin = UDP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fransferase; Glycogen biosynthesis; Acetylation; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O-LINKED (GLC. .) (BY SIMILARITY)
41F19CA7F09BF059 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 VKVVHYCAAGAKPWRFTGEEENMDREDIKM------LVKKWWDIYNDESL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.7%; Score 231; DB 1; Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACETYLATION (BY SIMILARITY). PHOSPHORYLATION (BY CAPK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 1e-12; 39; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF021343; AAB81219.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37247 MW;
Glycogenin-1 (EC 2.4.1.186).
GYG OR GYG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U96130; AAB53334.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 25.19
Matches 74; Conservative
                                                                                                                                                                                                                                                         glucosylglycogenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194
332 AA;
                                                                                                                                                                                                                                                                                                    (BY SIMILARITY)
                                                                                                    SEQUENCE FROM N.A.
                                                                        NCBI_TaxID-10116;
                                                                                                                                                                 cardiac tissue.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SELHFNRILKIGRF--PYMYENAKMMEQSLLNLAFSLDGWFPWTRLDPYYNGV---W-- 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 KSKYPLVVAVLPDVPEDHRKQLVDQGCVVKEIEP-----VYPPENQTEFAMAYYVINYS 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 KSKYPIHILALRGVDEWKIERFRKDGASVIVIDPIASSDIVYDTSSFSQEISARYEQMFS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----EAKLGPKPPLYFNAGMFVYEP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 -TKPDDDTVYHFNEDFKEYGASRSEFYPYLLAAVSDRGEHHSIPPEDTPYFNAGLMLIRP 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 NLSTYHNLLETVKIVPPTLF----AEQDFLNMYFK-DIYKP---IPPVYNLVLAMLWRH 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=972;
Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO S.POMBE SPEC4C3.08 AND SPEC4C3.09.
207 AKVVHFLGR-TKPWNYT---YNPQTKSVKCESQDPIVSHPEFLNLWWDTFTTNVL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94; Indels
                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 43.7 kDa protein C5H10.12C in chromosome I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 33 POTENTIAL.
371 AA; 43688 MW; 890BAD4A0E66379B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast),
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.1%; Score 165; DB 1;
25.0%; Pred. No. 6.2e-07;
tive 39; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
Glycogen synthesis initiator protein GLG2.
                                                                                                                                                                                                    Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         380 AA
                                                                                                                                                                                                371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 PENIELDQVKVVHYCAAGAKPWRFTGEE 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 PSIDERPLLKTAH-----GKFWNIGSSE 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z49811; CAA89962.1; -.
Hypothetical protein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 25.0%
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 QQCPDKVT----
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 YLDGDIQVFDNIDHLFDLP-NGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 KQLVDQGCVVKE---IEPVYPPENQTEFAMAYYVI-----NYSKLRIWEFVEYNKMI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 -----AFNTGVLLLIPDLDMATSLQDFLIKTVSIDG----ADQGIFNQFFNPICNYSK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 QEIALIRSLFKEIIIIEPLKDQEKSIEKNKANLELLKRPELSHTLLKARLWELVQFDQVL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---PEDHR 67
                                                                    SEQUENCE FROM N.A.
MEDLINE-96069371; PubMed-8524228;
MEDLINE-96069371; PubMed-8524228;
Cheng C., Mu J., Farkas I., Huang D., Goebl M.G., Roach P.J.;
Requirement of the self-glucosylating initiator proteins Glglp and Glg2p for glycogen accumulation in Saccharomyces cerevistae.";
Mol. Cell. Biol. 15:6632-6640(1995).
                                                                                                                                                                                                        Katsoulou C., Tzermia M., Tavernarakis N., Alexandraki D., "Sequence analysis of a 40.7 kb segment from the left arm of yeast chromosome X reveals 14 known genes and 13 new open reading frames including homologues of genes clustered on the right arm of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 LGPKPPLYFNAGMFVYEPNL----STYHNLLETVKIVPPTLFAEQDFLNMYF-----K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIYKPIPPV-----YNLVL-----AMLWRHPENIELDQVKVVHYCAAGAKPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVLHKVSPLMEWIRLPFTYNVTMPNYGYOSSPAM-----NFFQQHIRLIHFIGT-FKPW
                                                                                                                                                                                                                                                                             Yeast 12:787-797(1996).
-1- FUNCTION: SELF-GLUCOSYLATING INITIATOR OF GLYCOGEN SYNTHESIS.
                                                                                                                                                                                                                                                                                                        AS A PRIMER FOR THE ELONGATION REACTION CATALYZED BY GLYCOGEN
                Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 KRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36BDF556DEF397C0 CRC64;
                             Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE GLYCOGENIN FAMILY.
              Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.1%; Score 129.5; DB 1
Similarity 22.0%; Pred. No. 0.00077;
56; Conservative 50; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    618 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 29, Created)
(Rel. 32, Last sequence update)
  Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                             MEDLINE-96408771; Pubmed-8813765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                380 AA; 44546 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U25436; AAA91644.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X87371; CAA60818.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=S288C / FY1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycogen biosynthesis.
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                                                                                                                                                                                                                                                                                                                          SYNTHASE
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P36143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 QCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLF-----AEQ 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 DFLNMYF-----KDIYK----PIPPVYNLVLAMLWRHPE---NIELDQVKVVHYC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 GK-HKPWSLWSQKNFIKNE----YHDQWNEVYEEFKEEHQLNNEVSKPKISDSDKTETPE 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 KNILQSIYTKIVLVEPLNCQEESIQKNSENLALLE------RPELSFALI-----KA 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 GILNQFFNQNCCTDELVKDSFSREWVQLSFTYNVTIPNLGYQSSPAMNYFKPSIKLIHFI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 RLWELTQFEQVLYLDSD-----TLPLNKEFLKLFDIMSKQTTS----QVGAIA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---AKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GMYKKLAIATLLYSADYLPGVFALGHOVNKLLEEAGKKGDIETCLIVTTSLFNGTLSELA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                     and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            van Vliet-Reedijk J.C., Planta R.J.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: SELF-GLIOCOSYLATING INITIATOR OF GLYCOGEN SYNTHESIS.
AS A PRIMER FOR THE ELONGATION REACTION CATALYZED BY GLYCOGEN
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-96069371; PubMed-8524228;
Cheng C., Mu J., Farkas I., Huang D., Goebl M.G., Roach P.J.;
"Requirement of the self-glucosylating initiator proteins G191p of 31ycogen accumulation in Saccharomyces cerevisiae.";
Mol. Cell. Biol. 15:6632-6640(1995).
                                                                                                                                                                                Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56; Mismatches 122; Indels 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycogen biosynthesis.
SEQUENCE 618 AA; 69912 MW; E5422F6ACEDD9CDA CRC64;
                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE GLYCOGENIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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Glycogen synthesis initiator protein GLG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.7%; Score 122;
Best Local Similarity 18.5%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 GGEKRAYVTFLAGTGDYVKGVVGLAKGLRK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309 ----- XQQTLQQFIEALS 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 TITPVDAPPSNEPTTNQEIDTIS 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 139-480 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U25546; AAA91646.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z28283; CAA82136.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S38134; S38134.
SGD; S0001766; GLG1.
                                                                                                                                                                                                                                                         NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYNTHASE.
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95286551; PubMed=7768864; Antelmann H., Bernhardt J., Schmid R., Hecker M.; Antelmann H., Bernhardt J., Schmid R., Hecker M.; A gene at 333 degrees on the Bacillus subtilis chromosome encodes the newly identified sigma B-dependent general stress protein Gspa."; J. Bacteriol. 177:3540-3545(1995).

-!- INDUCTION: BY DIFFERENT STRESSES SUCH AS HEAT SHOCK AND SALT STRESS AND BY STRAYATION.

-!- SIMILARITY: TO H.INFLUBRABE H10259.

-!- SIMILARITY: TO LIPOPOLYSACCHARIDE 1,3-GALACTOSYLTRANSFERASE (RFAI) AND TO LIPOPOLYSACCHARIDE 1,2-GLUCOSYLTRANSFERASE (RFAI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequence of the sacS locus of Bacillus subtilis reveals the presence of two regulatory genes."; Gene 90:153-155(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene encoding a tyrosine tRNA synthetase is located near sacS in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95020537; PubMed-7934828;
Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,
Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,
Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,
Rapoport G., Danchin A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Bacillus subtilis genome project: cloning and sequencing of the
kb region from 325 degrees to 333 degrees.";
Mol. Microbiol. 10:371-384(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glaser P., Kunst F., Debarbouille M., Vertes A., Danchin A.,
Dedonder R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-90337338; PubMed-2116367;
Zukowski M.M., Miller L., Cosgwell P., Chen K., Aymerich S.,
                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                              01-MAY-1992 (Rel. 22, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                          286 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X52480; CAA36721.1; ALT_INIT.
EMBL; X73124; CAA51568.1; --
EMBL; M2933; AAA75337.1; --
EMBL; S99123; CAB1589.1; --
PTR; S16423; S16428.
Subtilist; BG10558; 959A.
Interpro; IPR002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
                                                                                                                                                                                                                                                                                                                                             Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION, AND SEQUENCE OF 1-28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92216127; PubMed=1806041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 110-286 FROM N.A.
                                                                                                                                                                                                    General stress protein A. GSPA OR IPA-12D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Seq. 1:251-261(1991).
                                      STANDARD;
                                                                                                                                                                                                                                                                             Bacillus subtilis,
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=QB1072;
                                      GSPA_BACSU
P25148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=168;
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GSPA_BACSU
                                      HDD BRREAD DRR BREAD DRR BRREAD DRR BRREAD DRR BRREAD DRR BRREAD D
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                                                                                                                                                 13;
                                                                                                                                                                                   62 VPEDHRKQLVDQ----GCVVKEIEPVYPPENQTEFAM-----AYVUINYSKLRIWEF 109
                                                                                                                                                                                                          110 VEYNKMIYLDGDIQVFDNIDHLFDLPNGQF--YAVMDCFCEKTWSHSPQYKIGYCQQCPD 167
                                                                                                                                                                                                                                                                                                                                168 KVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYHNLLETVKIV-----PPTLFA---EQDF 218
                                                                                                                                                                                                                                                                                                                                                                    148 MNVIDTGK-----YFNSGIMIIDFESWRKQNITE--KVINFINEHPDEDFLVLHDQDA 198
                                                                                                                                                                                                                                                                                                                                                                                                         219 LNMYFKDIYKPIPPVYN----LVL-----AMLWRHPENIELDQVKVVHYCAAGAKPWRF 268
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TWIL_YEAST STANDARD; PRT; 1251 AA.
004545; 003621;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 141.5 kDa zinc finger protein in TUBI-CPR3 intergenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                               62;
                                                                                                          6.1%; Score 110; DB 1; Length 286; 23.5%; Pred. No. 0.027; tive 39; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gentles S., Bowman S., Barrell B.G., Rajandream M.A.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brown D., Bowman S., Barrell B.G., Rajandream M.A.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: STRONG, TO YEAST ZMS1.
                 12 C -> A (IN REF. 4).
27 S -> V (IN REF. 4).
33522 MW; A282BE6E3B6518DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 TGEEENMDREDIKMLVKKWWDIYN 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 NTKHPYRDEYFHYMSYTKWNTIGN 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 469-1251 FROM N.A.
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InterPro; IPRO00822; Inf-C2H2.
Pfam: PFC00056; If-C2H2; Z.
PRINTS; PRC00048; ZINCFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z46660; CAA86657.1; -. EMBL; Z46373; CAA86497.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-488 FROM N.A.
                                                                                                 Ouery Match
Best Local Similarity 23.5%
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S288C / AB972;
                                  27
286 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4932;
Complete p
                                    CONFLICT
                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YML081W.
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YMI1_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLG_HRV1B STANDARD; PRT; 2157 AA.
P12916; Q89704; Q82106; Q82107; Q82108; Q82109; Q82110; Q82111;
Q82112; Q82113; Q82114; Q82115;
Q1-OCT-1989 (Rel. 12, Last sequence update)
10-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Genome polyprotein [Contains: Coat proteins VPI TO VP4; Core proteins P2A TO P2C, P3A; Genome linked protein VPG; Picornain 3C
[EC 3.4.22.28] (Protease 3C) (P3C); RNA-directed RNA polymerase P3D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATEMENT STATEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 LAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVIN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           779 LVQLIKISKLNYPLENFIKPPIESDHVLEYQDNPAVLNQFKAQYNTREQINRNFKYFILA 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                839 QSRIRIC-----HIDLLISNLFKSLVDFDCCF----HIDL 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                      70; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 YSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDLPNGQFYAVMD---CFCEKTWSHSPQY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88089537; PubMed=2826669;
MEDLINE=88089537; PubMed=2826669;
Hughes P.J., North C., Jellis C.H., Minor P.D., Stanway G.;
Hughes P.J., North C., Jellis C.H., Minor I.B.: molecular
Trelationships within the rhinovirus genus.";
J. Gen. Virtol. 69:49-58(1988).
I. FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN
O/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.
I. SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VPI, VP2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS. SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
SMART; SM00355; ZnF_C2H2; 2.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
Hypothetical protein; Nuclear protein; Zinc-finger; Metal-binding; DNA-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 KIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218 FLN--MYFKD----IYKPIPPVYNLVLAMLWRHPE--NIELDOVKVVHYCAAGAK--PWR
                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 1251;
                                                                                                                                                                                                                                                                                                                                                                                                               0.46;
ches 107; Indels
                                                                                                                                                                                                                                   89 112 C2H2-TYPE.
1251 AA; 141464 MW; 612F064177D6FF3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           977 M-----HSRPLVATMLKHWELLYIKNGGILALSDENLPIIN 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 FIGEEENMDREDIKMLVKKWWDIY------NDESLDYKN 300
                                                                                                                                                                                                                                                                                                                                                                            5.8%; Score 105; DB 20.6%; Pred. No. 0.46; Live 47; Mismatches
                                                                                                                                                                                           C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human rhinovirus 1B (HRV-1B)
                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 20.69
Matches 58; Conservative
                                                                                                                                                                                               83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VP3, AND VP4.
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                                                                                                                                                                                                                               ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                               ZN_FING
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POLG_HRV1B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1855 LKDELRK-----KE-----KE----------KISAGKTRVIEASSINDTILFR-- 1885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 N-----LVLAMLWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWW 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 IQVFDNIDHLFDL-PNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 DIYN--DES-----LDYKNVVIGDSHKKQQTLQQF-----IEALSEAGALQYVKAPS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 APEINTKLTVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPD 61
                                                                                                                                                                                                                                                   Polyprotein; Coat protein; Transleidae, Myristate.
Polyprotein; Coat protein; Core protein; Transleidae, Myristate.
RNA-directed RNA polymerase; Hydrolase; Thiol protease; Myristate.
2 69 COAT PROTEIN VP4 (PlA).
CHAIN 70 332 COAT PROTEIN VP2 (PlB).
CHAIN 333 570 COAT PROTEIN VP3 (PlC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 VPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 PLYFNAGMEVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIP-----PVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 2157;
                                                                                                                                                                                                                                                                                                                                                                                    GENOME-LINKED PROTEIN VPG (P3B).
                                                                                                                                                                                                                                                                                                                                                                                              PICORNAIN 3C.
RNA-DIRECTED RNA POLYMERASE P3D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           42DB649063B677B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       MYRISTATE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEASE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                           CORE PROTEIN P2C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.7%; Score 103.5;
                                                                                                                                                                                                                                                                                                                                   CORE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEASE
                                                                                                                                                                                                                     ProDom; PD001125; Cys-protease-3C; 1. ProDom; PD001274; Pico_P2B; 1. ProDom; PD001306; Pico_P2A; 1.
                                                                     Cys-protease-3C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                             InterPro; IPR000081; Pico_P2A.
InterPro; IPR001257; Pico_P2B.
InterPro; IPR001205; RNA_pol_P3D.
InterPro; IPR001676; Rhv.
Pfam; PF00548; Cys-protease-3C; 1.
                                                                                                                                                                                                           Pfam; PF00680; RNA_dep_RNA_pol; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55;
                                                                                    Pico_PlA.
                                                                                                                                                         PF02226; Pico_P1A; 1.
PF00947; Pico_P2A; 1.
PF01552; Pico_P2B; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.4%;
         EMBL; D00239; BAA00168.1;
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857
999
1094
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1493
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1697
2157
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                                                                                                                                                                                              Pfam; PF00073; rhv; 3.
                                                                     InterPro; IPR000199;
InterPro; IPR003138;
                        GNNY1B.
                                 HSSP; Q82122; 1AYN.
MEROPS; C03.007; -.
MEROPS; C03.021; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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2157
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858
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                       A28699;
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P27129;
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ACT_SITE
SEQUENCE
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                                                                                                                                                           Pfam;
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292 NDESLDYKNVV 302 | | | |::: 296 -DSPRDAKSII 305

QY Db

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 ONOLRITLYRINTDKLOCLPCTOVWSRAMYFRLFAFQLLGLTLDRLLYLDADVVCKGDIS 140
                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-KI2 / MG1655;
MEDLINE-94316500; PubMed-8041620;
Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
"Analysis of the Escherichia coli genome. V. DNA sequence of the
region from 76.0 to 81.5 minutes.";
Nucleic Acids Res. 22:2576-2586(1994).
-: CATALYTIC ACTIVITY: UDP-91ucose + lipopolysaccharide = UDP + D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----NKMIYLDGDIQVFDNID 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 HLFDLP-NGQFYAV---MDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|: || :| :| || :| || : SGV-VY-LDLKKWADAKLTEKALSILMSKDNVYKYPDQDVMNVLLKGMTLFLPREYNTIY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 TIKSELKDKTHQNYKKLITESTLLIHYTGA-TKPWHKWAIYPSVKYYKIALENSPWKD-- 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 AGMFVYEPNLSTYHNLLETVKIVPPTL-----FAEQDFLNMYFKDIYKPIPPVYNLVL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 AM-----LWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIY 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RYKHLLVQHHYISGIIAGVCYLCRKYYRK -> DINIF
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PIR; D42982; D42982.
EcoGene; EG11533; rfaJ.
InterPro; IPR002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
Lipopolysaccharide biosynthesis; Glycosyltransferase; Transferase;
                                                                                                                                                                                                                                          MEDLINE-92325066; PubMed-1624461; Pardel E., Parker C.T., Schnaiuman C.A.; Structures of the rial, rfaJ, and rfaS genes of Escherichia "Structures of the rial roles in assembly of the lipopolysaccharide coll K-12 and their roles in assembly of the lipopolysaccharide
                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.3%; Score 96.5; DB 1; Length 338; 21.5%; Pred. No. 0.49;
01-AUG-1992 (Rel. 23, Created)
01-CCT-1994 (Rel. 30, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Lipopolysaccharide_1/2-glucosyltransferase (EC 2.4.1.58).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91; Indels
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819428EA13F1959A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glucosyl-lipopolysaccharide.
.!- PATHWAY: LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: TO S.TYPHIMURIUM RFAJ AND TO RFAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 0.49
43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 OTEFAMAYYVINYSKL-----RIWEFVEY----
                                                                                                                                                                                                                                                                                                                                             Bacteriol. 174:4736-4745(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 QLLHLGLNGAVAAVVKDVEPMQEKAVS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 AA; 39040 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U00039; CAB34636.1;
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                                                                              RFAJ OR WAAJ OR B3626.
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                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                NCBI_TaxID=562;
                                                                                                       Escherichia col
                                                                                                                                             Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 273:1058-1073(1996).
--- FUNCTION: RESPONSIBLE FOR THE AMIDATION OF CARBOXYLIC GROUPS AT POSITION A AND C OF EITHER COBYRINIC ACID OR HYDROGENOBRYNIC ACID. NH(2) GROUPS ARE PROVIDED BY GLUTAMINE, AND ONE MOLECULE OF ATP
                                                                                                                                                                                                                                                                                                               ARAIN-JALU / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=8688087;

MEDLINE=96337999; PubMed=8688087;

Built C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Gocayne J.D., Sutton G.G., Blake J.A., Fitzderald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klomk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 AKLGPKPPLYFNAGM-FVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 PENQTEFAMAYYVINYSKLRIW-EFVEYNKMIYLDGDIQVFDNIDHLFDLPNGQFYAVWD 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 VF---LWEVNENYKKIAVAY----DKAFNFYYWDNFEALKENKAKIEFFSPLKDSEVPD 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 VKGVV-----GLAKGLRKAKSKYPLVVAVLPDVP--EDHRKQLVDQGCVVKEIEPVYP 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NH(2) GROUPS ARE PROVIDED BY GLUTAMINE, AND ONE MOLECULE OF ATP IS HYDROGENOLYZED FOR EACH AMIDATION (BY SIMILARITY). PATHWAY: COBALAMIN BIOSYNTHESIS. SIMILARITY: BELONGS TO THE COBB/COBQ FAMILY. COBB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002586; CbiA.
Pfam: PF01656; CbiA; 1.
Cobalamin biosynthesis; Porphyrin biosynthesis; Complete proteome.
SEQUENCE 443 AA; SOJOS WW, EA8D66D0FC9ED212 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.2%; Score 94.5; DB 1; Length 443; 20.6%; Pred. No. 1;
                                                                                                                                                                                                                 Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51; Mismatches 128; Indels
                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                 Probable cobyrinic acid A,C-diamide synthase
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                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U67583; AAB99432.1; -.
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                                                                                                                                                                                             jannaschii
                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity Matches 70; Conserv
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            NCBI_TaxID=2190;
                                                                                                                                                                          COBB OR MJ1421
                                                                                                                                                                                             Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR; MJ1421;
                                                                                                                                                                                                                                          Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       annaschii.
                                           COBB_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                               058816;
RESULT 13
                      COBB_METJA
                                           QΥ
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233 VYNL-VLAMLWRHPENIELDQVKVVHYCAAGAKPWRFTGEE-----ENMDREDIKMLVK 285
                                                                                                                                                                        343 VGLINCSAVMTKHVQGLSYVKAEFLEDCLIGRKGLKFKGHEFHYSKLVNIKEERFAYKIE 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-LT2;
MEDLINE-98204873; PubMed-9535865;
MEDLINE-98204873; PubMed-9535865;
MEDLINE-98204873; PubMed-9535865;
"The assembly system for the lipopolysaccharide R2 core-type of Escherichia coli is a hybrid of those found in Escherichia coli K-12 and Salmonella enterica. Structure and function of the R2 WaaK and WaaL homologs.";
J. Biol. Chem. 273:8849-8859(1998).
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PATHWAY: LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS.
SIMILARITY: TO E.COLI RETA AND TO RFAJ.
CAUTION: REF. 3 AND REF. 4 SEQUENCES DIFFER FROM THAT SHOWN DUE TO FRAMESHIFTS AND OTHER SEQUENCING ERRORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 18:6128-6128(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFAI_SALTY STANDARD; PRT; 337 AA.
191816; 068267;
01-FEB-1991 (Rel. 17, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Lipopolysaccharide 1,3-galactosyltransferase (EC 2.4.1.44).
RFAI OR WAAI OR STM3718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carstenius P., Flock J.-I., Lindberg A.; "Nucleotide sequence of rfaI and rfaJ genes encoding lipopolysaccharide glycosyl transferases from Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-1990) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                               286 KWWDIYND-ESLDYKNVVIGDSHKKQQTLQQFIEALSEAG 324
                                                                                                                                                                                                                                                                                                                       403 RGRGIINNLDGIFNGKVLAGYLHNHAVANPYFASSMVNFG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY SEQUENCE OF 198-337 FROM N.A.
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             entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                    67 FDSEDQQRFEALAKQYATQIVVYLIDCERLKSLPSTKNWTYATYFRFIIADYFSDKTDRV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 IYLDGDIQVFDNIDHLFDL--PNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Voll W., Voit R.; "Characterization of the gene encoding the hemocyanin subunit e from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schneider H.-J., Drexel R., Feldmaler G., Linzen B., Lottspeich F.,
                                                                                                                                       Stydene; SG10337; rfal.
InterPro; IPR002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
Lipopolysaccharide blosynthesis; Glycosyltransferase; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 AKLGPKPP----LYFNAGMFVYEPNLSTYHN-----LLETVKIVPPTLFAEQDFLNMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91060544; PubMed=2246235; Voit R., Feldmater-Fuchs G.; Nathrepood hemocyanins. Molecular cloning and sequencing of cDNAs encoding the tarantula hemocyanin subunits a and e.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukāryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Theraphosidae; Aphonopelma.
NCBL_TaxID=29932;
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                                                                                                                                                                                                                                                                                                                          5.1%; Score 93.5; DB 1; Length 337; 20.3%; Pred. No. 0.88; ive 36; Mismatches 83; Indels 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 FKDIYKPIPPVYNLVLAMLWRHPENI -- ELDQVKV-VHYCAAGAKPWRFTG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 LVNKARFVDKKFNTQFSLNYELKDSVINPVDAETVFVHYIGP-TKPWHSWG 276
 Usage by
                                                                                                                                                                                                                                                     -> Q (IN REF. 1).
6DB1FA1531AE25F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  84 YPPENQTEF -----AMAYYVINYSKLRI-----WEFVEY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the tarantula Eurypelma californicum.";
Proc. Natl. Acad. Sci. U.S.A. 87:5312-5316(1990).
                                                                                                                                                                                                                                    -> RE (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
modified and this statement is not removed.
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                                                                                      EMBL; AE008873; AAL22577.1; -.
EMBL; X53847; CAA37841.1; ALT_FRAME.
PIR; S12097; S12097.
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                                                                     EMBL; AF026386; AAC16412.1; -.
                                                                                                                                                                                                                                                                       337 AA; 38905 MW;
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 20.33
Matches 47; Conservative
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                                                                                                                                                                                                                   COMPLICT 125
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623 AA; 71545 MW; E411052A80814004 CRC64;

SEQUENCE

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                                                                             "Tarantula hemocyanin mRNA. In vitro translation, cDNA cloning and nucleotide sequence corresponding to subunit e."; sequence corresponding to subunit e."; Eur. J. Biochem. 159:23-29(1986).
-i. FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                                                                                                                                             ARTHROPODS.
SUBUNIT: TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN DIFFERENT CHAINS IDENTIFIED
                                                                                                                                                                                                                                                                    -:- SUBCELLULAR LOCATION: Extracellular.
-:- SIBCELLULAR LOCATION: Extracellular.
-:- TISSUE SPECIFICITY: HEMOLYMPH.
-:- MISCELLANBOOGS: THE TWO COPPER IONS BOUND EACH HAVE 3 NITROGEN LIGANDS (PRESUMABLY CONTRIBUTED BY HIS RESIDUES) AND SHARE A BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN ADDITION TO BINDING OXYGEN.
-:- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PRO0187; HEMOCYANIN.

PROSITE; PS00209; HEMOCYANIN.1; 1.

PROSITE; PS004209; HEMOCYANIN.1; 1.

PROSITE; PS004409; TYROSIANSE.2; 1.

Transport; Oxygen transport; Copper; Glycoprotein; Hemolymph.

INIT.MET 168 COPPER 1 (PROBABLE).

METAL 172 172 COPPER 1 (PROBABLE).

METAL 179 199 COPPER 1 (PROBABLE).
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N-LINKED (GLCNAC. .) (PRO C -> D (IN REF. 2).
C -> D (IN REF. 2).
R -> K (IN REF. 2).
A -> H (IN REF. 2).
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A -> H (IN REF. 2).
C -> D (IN REF. 2).
A -> H (IN REF. 2).
C -> D (IN REF. 3).
Biol. Chem. 265:19447-19452(1990)
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SEQUENCE OF 74-599 FROM N.A.
MEDLINE=86300721; Pubmed=3017715;
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InterPro; IPR000896; Hemocyanin.
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                                                                                                                                                                     80 TFVNEGLFVYAVSVALLHR--DDCKGIVVPA-----IQEIFPDRFVPTETI-NLAVKE 129
                                                                        123 QVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQ-YKIGYCQQCPDKVTWPEAKLGPKPP 181
                                    Indels 31; Gaps
                                                                                               241 LWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMD--REDIKMLVKKW-WDI 290
                                                                                                                                                                                                                                                             130 AANHP-----DQDISVHVVETG----NILDEEYKLAYFKEDVGTNAHHWHI 173
 Length 623;
                                      73;
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Score 93.5; DB Pred. No. 1.9;
                                    24; Mismatches
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 Query Match
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OM protein - protein search, using sw model

Run on: July 2, 2002, 12:14:44; Search time 48.67 Seconds (without alignments) 1190.740 Million cell updates/sec

Title: US-09-810-506-2
Perfect score: 1816
Sequence: 1 MAPEINTKLTVPVHSATGGE......FIEALSEAGALQYVKAPSAA 335

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
1	1816	100.0		0.1	Q9FXB2	Q9fxb2 arabidopsis
7	1516.5	83.5		10	080518	080518 arabidopsis
٣	1390.5	76.6		10	022893	022893 arabidopsis
4	1388	76.4	341	10	Q9XEJ7	Q9xej7 brassica na
Ŋ	1345.5	74.1		10	Q9XGG4	Q9xgg4 pisum sativ
9	1319	72.6		10	040710	040710 oryza sativ
7	1298.5	71.5		10	022693	022693 arabidopsis
ω	1284.5	70.7		10	Q9XGN4	Q9xgn4 ajuga repta
6	1219	67.1		10	094511	094511 arabidopsis
10	1216.5	67.0		10	Q9XGN3	Q9xqn3 ajuga repta
11	1198.5	0.99		10	601S60	Q9stq9 arabidopsis
12	1198	0.99		10	Q9FFA1	Q9ffal arabidopsis
13	1110	61.1		10	080766	080766 arabidopsis
14	1053.5	58.0		10	Q947G8	Q947g8 lycopersico
15	763.5	42.0		10	Q9SPE1	Q9spel vitis ripar
16	258.5	14.2	_	10	080649	080649 arabidopsis

09w2j6 drosophila 0940b5 arabidopsis 091sb1 arabidopsis 091s23 arabidopsis 043061 schizosacch 094hg3 oryza sativ 05324 rhodobacter 098zb0 arabidopsis 02529 caenorhabdi 09595 caenorhabdi 091805 printobin 091805	
5 09W2J6 10 0940B5 110 0940B5 110 09F237 3 043061 110 094HG3 12 095234 110 095280 12 095297 12 091896 12 091896 12 091896 12 091896 13 091896 14 091896 15 091896 16 091896 17 091896 18 091896 18 091896 19 091896 10 091896 10 091896 11 091896 12 091896 13 091896 14 091896 15 091896 16 091897 17 091896 18 091897 19 091897 19 091897 19 091897 19 091897 19 091897 19 091897 19 091897	
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAPEINTKLTVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLP 60
Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Kazlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nayen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tarq G.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
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Federspiel N.A., Palm C.J., Conway A.B., Kurtz D.B., Conway A.R., Au M., Araujo R., Buehler E., Dewar K., Feng J., Kim C., Li Y., Oji O., Osborne B.I., Shinn P., Sun H., Toriumi M., Vysotskaia V.S., Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 LWRHPENIELDOVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLDYKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAM
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1816; DB 10; Length 335; 100.0%; Pred. No. 1.8e-161;
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                                                                                                                                                                                                            Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AC009323; AAG09103.1; -. EMBL; AYOS04318; AAL5412.1; -. EMBL; AYOS0410; AAK01426.1; -. EMBL; AYOS0410; -. EMBL; AYOS0410
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Last annotation update)
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01-NOV-1998 (
01-DEC-2001 (
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STRAIN-CV. COLUMBIA;
MEDLINEASON SHART; Pubmed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                                                          DIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                      DVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 DIQVFENIDHLFDLPDGNFYAVKDCFCEKTWSHTPQYKIGYCQQCPDKVTWPESELGPKP 174
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                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                  PLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEODFLNMYFKDIYKPIPPVYNLVLAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
                                                                                                                                                                                                 DB 10; Length 334;
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                                                                                                                                                                                                                                       24; Indels
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinn Ecker J., Theologis A., Davis R.W.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC003970; AAC33195.1; -.
EMBL; AF370546; AAK48973.1; -.
EMBL; AF370546; AAK48973.1; -.
EnterPro; IPR002495; Glycosyl_Laransf_8.
Pfam; PF01501; Glyco_transf_8; 1.
SEQUENCE 334 AA; 38677 MW; 0D09CA497B392BA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lin X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE GALACTINOL SYNTHASE.
AT2G47180 OR T8113.2/AT2G47180.
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                                                                                                                                                                                                                   Best_Local Similarity 80.9
Matches 275; Conservative
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 VYNLVLAMLWRHPENVELGKVKVVHYCAAGSKPWRYTGKEANMEREDIKMLVKKWWDIYD 300
      Camada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyem M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R., Theologis A., Full Length cDNA of gene T8113.2/At2g47180 (GI:2275196)."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AV065139, AALO7218.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 PLVVAVLPDVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEFVEY 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VYNLVLAMLWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYN 292
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAPEI-----NTKLTVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAPGLTQTADAMSTVTITKPSLPSVQDSDRAYVTFLAGNGDYVKGVVGLAKGLRKVKSAY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Georges F., Bock C.A., Hussain A.K., Yan W., Keller W.A.;
"Cloning and Characterization of a Full Length cDNA for Galactinol
Synthase from Brassica napus.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF106954; AAD26116.1;
ThterPro: IPR002495; Glycosyl_transf_8.
Pfam: PF01501; Glycosyl_transf_8;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EAKLGPKPPLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPP
                                                                                                                                                                                                                                                                                                                                                   Query Match 76.6%; Score 1390.5; DB 10; Length 344; Best Local Similarity 74.7%; Pred. No. 1.1e-121;
                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                           47; Indels
                                                                                                                                                                                                                                                  Interpro; IPR002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
SEQUENCE 344 AA; 39596 MW; 46784Ea16DBD3A46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 341 AA; 39059 MW; 12ED74936583D157 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 DESLDYKN-VVIGDSHKKQQTLQQFIEALSEAGALQYVKAPSAA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341 AA
                                                                                                                                                                                                                                                                                                                                                                                             31; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                             Matches 257; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3708;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
NCBI_TaxID=3888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 DVPEEHREMLESQGCIVREIQPVYPPENQTQFAMAYYVINYSKLRIWEFVEYSKMIYLDG 119
                                                                                                                                  67 RKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIMEFVEYNKMIYLDGDIQVFD 126 |: ||:|||:||:||||||||:: | 72 RRVLVEQGCIVREIEPVYPPENQTQFAMAYYVINYSKLRIMKFVEYSKMLYLDGDIQVYE 131
                                                                                                                                                                                                                                                                                                                                                            187 GMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAMLWRHPE 246
                                                                                                                                                                                                                                                                                          247 NIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLDYKNVVIGDS 306
                                                                                                                                                                                                    127 NIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Gaps
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                                                                  7 TKLTVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDH 66
                                                                                   DB 10; Length 334;
                                8;
 Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43; Indels
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones R.G., Harrison C.J., Hedley C.L.;
"Cloning of Galactinol synthase from Pea embryo.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ248H5; CAB51130.1;
InterPro; IPR002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8.
Transferase; Glycosyltransf_8.
ETABSE Glycosyltransf_8.

Fransferase; Glycosyltransf_8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Carbon partitioning in developing pea embryos.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OJANUA, 1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE GALACTINOL SYNTHASE (EC 2.4.1.123).
 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.8e-117;
76.4%; Score 1388; DB 10; 76.4%; Pred. No. 1.9e-121; iive 35; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.1%; Score 1345.5; 72.9%; Pred. No. 1.8e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              307 HKKQQ--TLQQFIEALSEAGALQYVKAPSAA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-EMBRYO (AXIS AND COTYLEDONS);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=EMBRYO (AXIS AND COTYLEDONS);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pisum sativum (Garden pea).
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                                   Matches 253; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                   Best Local Similarity
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   Query Match
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022693
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            181 PLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAM 240
                                                                                             241 LWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLDYKN 300
                                                                                                                                                                                                                                                                                                                                                                                                                       analysis and expression of water stress, and cDNA sequence analysis and expression of water stress-regulated genes in rice."; Plant Mol. Biol. 26:339-352(1994).
EMBL, D26537; BAA05538.1; -.
InterPro; IPR002495; Glycosyl_transf_8.
Ffam; PF01501; Glyco_transf_8; 1.
SEQUENCE 328 AA; 37698 MW; D87DECDAA7AF98B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 DVPGEHRRKLVEQGCVVREIQPVYPPESQTQFAMAYYVINYSKLRIWEFVEYERRWYKLDA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 DIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 PLYFNAGMEVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 LWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLDYKN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 LWHPPENVDLDQVKVVHYCAAGSKPWRFTGKEENMNREDIKMLVKRWWDIYNDESLDYKE 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAPEINTKLTVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 MGPNVSSE----KKALAAAKRRAYVTFLAGDGDYWKGVVGLAKGLRRVRSAYPLVVAVLP 57
DIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKP
                                                                                                                                                                                                                                                                                                                   Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.6%; Score 1319; DB 10; Length 328; 71.0%; Pred. No. 5.2e-115;
                                                                                                                                                                                                                                                                                                    Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidee; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
                                                                                                                                             301 VVIGDSHKKQQTLQQ-FIEALSEAGALQYVKAPSAA 335
                                                                                                                                                            VVIGDSHKKQQTLQQFIEALSEAGALQYVKAPSAA 335
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                                                                                                                                                                                                                                 328 AA
                                                                                                                                                                                                                                                                                                                                                                                                              Takahashi R., Joshee N., Kitagawa Y.,
"Induction of chilling resistance by water
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Pred. No. 5.2e
41; Mismatches
                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seque
01-DEC-2001 (TrEMBLrel. 19, Last annot
WSI76 PROTEIN INDOCED BY WATER STRESS.
                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=SOMEWAKE;
MEDLINE=95036005; PubMed=7948880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238; Conservative
                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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Best Local S
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Q40710;
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121
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 LDGDIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237
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EMBL, AC002292; AAB71970.1; --InterPro; IPR002495; Glycosyl_transf_8.

Pfam. PF01501; Glyco_transf_8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 VLPDVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIY 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAMLWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLD 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAPEISVNPMYLSEKAHQAP--PRRAYVTFLAGNGDYVKGVVGLAKGLRKVKSAYPLVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ajuga reptans (bugle).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Asteridae, euasterids I; Lamiales; Lamiaceae; Ajuga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAPEINTK---LIVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKPPLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.5%; Score 1298.5; DB 10; Length 334; 70.7%; Pred. No. 4.4e-113; ive 35; Mismatches 52; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01501; Glyco_transf_8; 1.
SEQUENCE 334 AA; 38511 MW; 591D3D441F01FA75 CRC64;
                                              Created)
Last sequence update)
Last annotation update)
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334 AA
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                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
PRT;
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19,
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                                              (TrEMBLrel. C (TrEMBLrel. C (TrEMBLrel. 1
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PRELIMINARY;
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NCBI_TaxID=38596;
[1]
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
                                                                                                                             2 PROTEIN.
                                                                      01-JAN-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 241;
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Best Local 9
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Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Ouach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 CAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLDYKNVVIGDSHKKQQT--LQQF 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 EIEPIYPPANQIQFAMAYYVINYSKLRIWNFEEYSKWYLDADIQVYENIDHLLDTPDGY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTY 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 HNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAMLWRHPENIELDQVKVVHY 258
                                                                                                                                                                                                                                                                                                                                                                                                                                   EIEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDLPNGQ 138
                                                                                                                                                                                                                                                                                                                                                                         20 GAKKGYVTFLAGNGDYVKGVVGLAKGLRKVKSAYPLVVAILPDVPEEHRELLRSQGCIVK 79
                MEDINE-20224020; PubMed-10758476;
Sprenger N., Keller F.;
"Allocation of raffinose family oligosaccharides to transport and
storage pools in Ajuga reptans: the roles of two distinct galactinol
                                                                                                                                                                                                                                                                                                                  7; Gaps
                                                                                                                                                                                                                                                                                                                                                       19 GEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQGCVVK 78
                                                                                                                                                                                                                                                                         Ouery Match 70.7%; Score 1284.5; DB 10; Length 333; Best Local Similarity 73.0%; Pred. No. 8.8e-112; Matches 233; Conservative 38; Mismatches 41; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Arabidopsis cDNA clones.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AF412094 AAL06547.1;
SEQUENCE 221 AA; 25759 MW; 30D65575CB2D706C CRC64;
                                                                                                                                                        InterPro; IPR002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
Transferase; Glycosyltransferase; Glycosyltransferase; Glycosyltransferase; SEQUENCE 333 AA; 37881 MW; B3D575F9084DFF6B CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                 Plant J. 21:249-258(2000).
EMBL; AJ237693; CAB51533.1; -.
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SEQUENCE FROM N.A.
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67.1%; Score 1219; DB 10; Length 221;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 INYSKLRIWEFVEYSKMIYLDGDIQVFENIDHLFDLENGYFYAVMDCFCEKTWSHTPQYQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 LNMYFKDIYKPIPPVYNLVLAMLWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDRE 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 KIGPKPPLYFNAGMFVYEPNLSTYHNILETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVY 120
                                                                                                                                                                                            Gaps
                                             115 MIYLDGDIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEA 174
                                                                                                            175 KLGPKPPLYENAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVY 234
                                                                                                                                                                         NLVLAMLWRHPENIELDQVKVVHYCAAGARPWRFTGEEENMDREDIKMLVKKWWDIYNDE 294
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               Gaps
                                                              storage pools in Ajuga reptans: the roles of two distinct galactinol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE=20224020; PubMed=10758476;
Sprenger N., Keller F.;
"Allocation of raffinose family oligosaccharides to transport and
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GALACTINOL SYNTHASE, ISOFORM GOLS-2 (EC 2.4.1.123) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             // Match 67.0%; Score 1216.5; DB 10; Lengt
Local Similarity 75.4%; Pred. No. 1.7e-105;
nes 224; Conservative 29; Mismatches 39; Indels
               Indels
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                                                                                                                                                                                                                                                         SLDYKNVVIGDSHKKQQTLQQFIEALSEAGALQYVKAPSAA 335
100.0%; Pred. No. 6.7e-106; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                         292 AA
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EMBL; AJ237694; CAB51534.1; -.
InterPro; IPR002495; Glycosyl_transf_8.

Fransferase; Glycosyltransf_8; 1.

Transferase; Glycosyltransferase.
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                221; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ajuga reptans (bugle).
 Best Local Similarity
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T13D8.32 PROTEIN.
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01-NOV-1998 (
01-DEC-2001 (
         -MAR-2001
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Best Local S
Matches 221
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                                                                                                                                            Rosidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 LGPKPPLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAAEQDFLNMYFKDIYKPIPPVYN 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 KRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKEI 80
                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidieurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 361;
                                                                                                                                                                                       SEQUENCE FROM N.A.
Bevan M., Koetter P., Hempel S., Entian K.-D., Bancroft I.,
Mewes H.W., Mayer K.F.X., Schueller C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61; Indels
                                                                                                                                                                                                                                                                                                                                                 EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO49171; CAB39954.1;
EMBL; ALI61564; CAB79480.1;
InterPro; IPR007495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
                                                                                                                                                                                                                                                          EU Arabidopsis sequencing project;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                  41906 MW; F10846E37ACF95F1 CRC64;
                                                                         01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 41.9 KDA PROTEIN.
T25K17.60 OR AT4G26250.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.0%; Score 1198.5; DB 1(65.0%; Pred. No. 1.1e-103; ive 31; Mismatches 61;
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                                                                                                                                                                                                                                                                                                         Rose M., Hempel S., Entian K.-D., Mewes H.W.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
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                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
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                                        PRELIMINARY;
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5. I. Sequence
                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; <u>B</u>rassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 PLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 LWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLDYKN 300
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                              Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M., Miyajima N., Tabata S.; "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequenc features of the 1.6 Mb regions covered by twenty physically assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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STRAIN=CV. COLUMBIA;
Vysotskaia V.S., Schwartz J.R., Kwan A., Toriumi M., Yu G., Oji, O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MTMTVEKRIEADVTVSHEGVERAYVTFLAGNKDYWMLVVGLAKGLRKVKSAYPLVVATLP
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EMBL; AB005244; BAB10052.1; -.

INTECPPO; IPRO02495; GIycosyl_transf_8.

Pfam; PFO1501; GIyco_transf_8; 1.

SEQUENCE 333 AA; 38472 MW; EEBBEFB82FBBEAA3 CRC64;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.0%; Score 1198; DB 10; 66.0%; Pred. No. 1.1e-103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 FV -- ETESKLNPVTATLASKKLVGDVLTSLAPSAA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                345 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 1.16 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                         STRAIN=COLUMBIA;
MEDLINE=97471969; Pubmed=9330910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08,
08,
19,
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                                                                                  GALACTINOL SYNTHASE.
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Liu S., Li J., Araujo R., Au M., Brendel V., Buehler E., Conway A.B., Conway A.R., Dewar K., Feng J., Kim C., Kurtz D., Li Y., Palm C.J., Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 KPPLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 AMLWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLDY 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGDIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Downle B., Dahal P., Nonogaki H., Gurusinghe S., Yim K., Fukanaga K., Alvarado V., Bradford K.J.;
Galactinol synthase gene expression in tomato seeds.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF311943; AAL26804.1: -
Transferase; Glycosyltransferase; Stycosyltransferase; Stycosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 EKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                          "Arabidopsis thaliana chromosome 1 BAC T13D8 sequence."; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                    STRAIN=CV. COLUMBIA;
Theologis A.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                 EMBL; AC004473; AAC24075.1; -
InterPro; IPR002495; Glycosyl_transf_8.
Pfam, PF01501; Glyco_transf_8 1.
SEQUENCE 345 AA; 39372 WW; B4EDDE0FDA075E69 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE GALACTINOL SYNTHASE I (EC 2.4.1.123).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.1%; Score 1110; DB 10;
59.9%; Pred. No. 1.9e-95;
tive 46; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 KNVVIGDSHKKQQTLQQ--FIEALSEAGALQYVKAPSAA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 KPKSPAD---LEATVLESTIIASVTEAPLSYSPAAPSAA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 59.99
Matches 203; Conservative
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Q947G8
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Vitaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 QLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDGDIQVFDNI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 LDGDIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLG 177
                                                                                                                                                                                   117 LDGDMOVFENIDHLFELPDKYLYAVADCICDM-----YGEPCDEVLPWPK-ELG 164
                                                                                                                                                                                                                    PKPPLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLV 237
                                                                                                                                                                                                                                    238 LAMLWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLD 297
                                                                                                                                                                                                                                                                                                 225 LAMLWRHPEKIEVNKAKAVHYCSPGAKPWKYTGKEEHMDREDIKMLVKKWWDIYNDTTLD 284
                                                                                           LPDVPEDHRKQLVDQGCVVKEIEPVYPP-ENQTEFAMAYYVINYSKLRIWEFVEYNKMIY 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39; Gaps
                               1 MAPEI -- NTKLTVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAV 58
                                             15 SATGGEK-----RAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 DHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.0%; Score 763.5; DB 10; Length 213; 80.9%; Pred. No. 2.4e-63; cive 12; Mismatches 15; Indels 7;
 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li X.-Z., McKersie B.D.;
"Freezing tolerance in gape flower buds.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF178569; AAD55726.1; -.
InterPro; IPR002495; Glycosyl_transf_8.
Pfam: PF01501; Glyco_transf_8; 1.
NON_IER
                                                                                                                                                                                                                                                                                                                                                                298 YKNVVIGDSHKKQQTLQQFIEALSEAGA------LQYVKAPSAA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6D008A67FF729EEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Mismatches
   48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 144; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=96939;
    202;
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    Matches
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Score 1053.5; DB 10; Length 318; Pred. No. 3.3e-90;

58.0%; 58.4%;

Best Local Similarity

Query Match

Job time: 376 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 2, 2002, 12:09:33 ; Search time 29.88 Seconds (without alignments) 1077.307 Million cell updates/sec

US-09-810-506-2 1816 1 MAPEINTKLTVPVHSATGGE......FIEALSEAGALQYVKAPSAA 335 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID 1 1816 100.0 335 2 G96607 probable galactino hypothetical prote probable galactino hypothetical prote probable galactino hypothetical prote probable galactino wall by a constant of the consta	Result		% Query			SUMMARIES		, A A
1816 100.0 335 2 G96607 1516.5 83.5 334 2 F86226 1319.5 72.6 328 2 T07610 1298.5 71.5 334 2 H96629 1198.5 66.0 361 2 T06009 1110 6.1 1 201 2 T0244 235.5 13.0 332 1 A4594 235.5 12.8 557 2 T40489 205.5 11.3 333 1 JC4695 205.5 11.3 372 2 T40489 205.5 11.3 372 2 T40489 205.5 11.3 372 2 T40489 197 10.8 429 2 T31001 157.5 8.7 404 2 S55490 157.5 8.7 444 444 137 7.3 376 2 H94688 134 7.3 376 2 H9488 134 7.3 376 2 H9488 134 7.3 376 2 H9488 137 7.3 380 2 S55176 118 6.5 114 2 S58330 110 6.1 491 2 S58330	No.	Score	Match	Length	DB	ΠD	Description	Ŕ
1516.5 83.5 334 2 F86226 1390.5 76.6 334 2 F86226 1319 72.6 328 2 T07610 1298.5 71.5 334 2 H96629 1198.5 66.0 361 2 T06009 1110 6.1 1 201 2 T00444 235.5 13.0 33.1 JC4695 235.5 12.4 372 2 H96590 205.5 11.3 33.1 JC4695 205.5 11.3 33.2 1 A45944 235.5 12.4 372 2 T40489 205.5 11.3 330 2 T05984 197 10.8 429 2 T31001 157.5 8.7 546 2 G86221 147.5 8.7 546 2 G86221 140. 7.7 470 2 A84772 131 7.2 406 2 H95205 129.5 7.1 380 2 S55176 118 6.5 114 2 JC6077 110 6.1 491 2 S58330	7	1816	100.0	/	7	G96607	probable qalactino	که رژ
1390.5 76.6 344 2 A84912 probable gala 1390.5 76.6 348 2 TO610 WSIT6 protein 1298.5 71.6 328 2 TO610 MSIT6 protein 1298.5 71.6 34 2 TO609 hypothetical 110 61.1 345 2 TO6295 hypothetical 110 61.1 345 2 TO6295 hypothetical 128.5 14.2 120.1 2 TO6444 glycogenin glycog	7	1516.5	83.5		7	F86226	hypothetical prote	A;
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1298.5 71.5 334 2 H96629 hypothetical l198.5 66.0 361 2 T06009 hypothetical l198.5 66.0 361 2 T06099 hypothetical l198.5 66.0 361 2 T00444 phypothetical section 61.2 1201 2 T00444 phypothetical l235.5 13.0 33.1 1 JC4695 phypothetical l235.5 12.4 372 2 T40489 phypothetical hypothetical l25.5 11.3 260 2 A45729 phypothetical hypothetical l197 10.8 429 2 T31001 phypothetical l197 10.8 429 2 T31001 phypothetical l165 9.1 371 2 S52490 phypothetical l167.5 8.7 404 2 C95206 phypothetical l167.5 8.7 404 2 C95206 phypothetical l167.5 8.7 404 2 A74733 phypothetical l147.5 8.7 470 2 A84772 phypothetical l143.5 7.3 398 2 G95205 phypothetical l140 7.7 470 2 A84772 phypothetical l180 7.7 470 2 A84772 phypothetical l180 7.1 380 2 S55176 gG22 protein l180 6.1 1286 2 S16423 probable members l10 6.1 491 2 S58330	4	1319	72.6		7	T07610	WSI76 protein - ri	
1198.5 66.0 361 2 T06009 hypothetical 258.5 14.2 1201 2 T06444 hypothetical hypothetical 241 13.3 33.1 JC4695 hypothetical hypothetical 33.1 JC4695 glycogenin gl 255.5 12.4 372 2 T40489 hypothetical 325.5 11.3 260 2 A45729 hypothetical 197 10.8 429 2 T31001 hypothetical 197 10.8 429 2 T31001 hypothetical 194 10.7 300 2 T2225 hypothetical 157.5 8.7 404 2 C92206 hypothetical 157.5 8.7 546 2 G86221 hypothetical 157.5 8.7 546 2 G86221 hypothetical 147.5 7.9 301 2 T24773 hypothetical 147.5 7.9 301 2 T24773 hypothetical 147.5 7.9 301 2 T24773 hypothetical 147.5 7.9 406 2 H95205 glycosyl tran 138 7.3 398 2 G95205 glycosyl tran 138 7.3 398 2 G95205 glycosyl tran 129.5 7.1 380 2 S55176 GLG2 protein 7129.5 7.1 380 2 S55176 GLG2 protein 110 6.1 491 2 S58330 probable members	S	1298.5	71.5	334	~	Н96629	hypothetical prote	
1110 61.1 345 2 T02295 hypothetical 258.5 14.2 1201 2 T00444 hypothetical 31 1 JC6695 32 14.2 1201 2 T00444 hypothetical 241 13.3 13 1 JC6695 325.5 13.0 332 1 A45094 hypothetical 255.5 12.8 557 2 H96590 hypothetical 305.5 11.3 260 2 A4729 hypothetical 31 2 T05984 hypothetical 194 10.7 300 2 T25275 hypothetical 194 10.7 300 2 T25275 hypothetical 157.5 8.7 546 2 G86221 hypothetical 157.5 8.7 546 2 G86221 hypothetical 147.5 7.9 321 2 T24733 hypothetical 147.5 7.9 321 2 T24733 hypothetical 147.5 7.9 321 2 T24773 hypothetical 134 7.4 376 2 H4688 hypothetical 134 7.4 376 2 H4688 hypothetical 136 7.3 398 2 G95205 g1ycosyl tran 129.5 7.1 380 2 S55176 hypothetical 136 7.2 14068 hypothetical 137 7.2 406 2 H95205 g1ycosyl tran 110 6.1 491 2 S58330 probable members 110 6.1 491 2 S58330 probable members 110 6.1 491 2 S58330	9	1198.5	0.99	361	7	T06009	hypothetical prote	
258.5 14.2 1201 2 T00444 hypothetical 241 13.3 33.3 1 JC4695 glycogenin gl 235.2 12.8 557 2 H96590 hypothetical 225.5 12.4 372 2 T40489 hypothetical hypothetical 205.5 11.3 260 2 A45729 hypothetical 197 10.8 429 2 T31001 hypothetical 197 10.8 73 2 T22575 133 2 T05984 hypothetical 197 10.8 429 2 T31001 hypothetical 157.5 8.7 546 2 G86221 hypothetical 157.5 8.7 546 2 G86221 hypothetical 147.5 8.1 442 2 A77433 hypothetical 147.5 8.1 442 2 T4473 hypothetical 140° 7.7 470 2 A84772 hypothetical 134 7.4 376 2 T40488 hypothetical 132 7.3 398 2 G95205 glycosyl tran 129.5 7.1 380 2 S55176 fly 2 GGZ protein 129.5 7.1 380 2 S55176 fly 3 general stress 110 6.1 491 2 S58330 probable members.	7	1110	61.1	345	~	T02295	hypothetical prote	
241 13.3 33.1 JG4695 235.5 13.0 33.2 I A45094 225.5 12.4 372 2 H96590 205.5 11.3 260 2 A45729 205.5 11.3 260 2 A45729 205.5 11.3 2 60 2 A45729 205.6 11.3 2 60 2 A45729 205.7 11.3 2 60 2 A45729 205.8 11.3 2 C0984 207 10.8 429 2 T31001 208 1 420 2 T32575 208 208 208 208 208 208 208 208 208 208	80	258.5	14.2	1	7	T00444	hypothetical prote	
235.5 13.0 33.2 1 A45094 hypothetical 225.5 12.8 557 2 H96590 hypothetical hypothetical 205.5 11.3 260 2 A4729 hypothetical hypothetical 197 10.8 4.29 2 T30394 hypothetical 194 10.7 300 2 T32575 14.4 4.2 2 T31001 hypothetical 194 10.7 300 2 T32575 15.5 8.7 546 2 G86221 hypothetical 157.5 8.7 546 2 G86221 hypothetical 147.5 8.7 546 2 G86221 hypothetical 147.5 7.7 470 2 A84772 hypothetical 140 7.7 470 2 A84772 hypothetical 127.5 8.1 442 2 T24773 hypothetical 134 7.4 376 2 H4048 hypothetical 134 7.4 376 2 H4048 hypothetical 132 7.3 398 2 G95205 glycosyl tran 129.5 7.1 380 2 G95205 glycosyl tran 118 6.5 114 2 JC6077 general stress 110 6.1 491 2 S58330 probable members	6	241	13.3		-	JC4695	glycogenin glucosy	٥
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225.5 12.4 372 2 T40489 hypothetical 205.5 11.3 260 2 A45729 glycogenin ho 206 11.3 33 2 T05984 hypothetical 197 10.8 429 2 T31001 hypothetical 194 10.7 300 2 T22275 hypothetical hypothetical 165 9.1 370 2 S52490 hypothetical 157.5 8.7 404 2 C95206 protein F7019 147.5 8.7 442 2 A71473 hypothetical 147.5 8.7 470 2 A84772 hypothetical 140 7.7 470 2 A84772 hypothetical 110 7.7 470 2 A84772 hypothetical 132 7.3 398 2 G92205 glycosyl tran 129.5 7.1 380 2 S55176 GLG2 protein 129.5 7.1 380 2 S55176 GLG2 protein 110 6.1 286 2 S16423 probable memb 110 6.1 491 2 S58330 probable memb	11	232	12.8		7	н96590	hypothetical prote	ac D
205.5 11.3 260 2 A4729 giyogenin ho 205 11.3 33.3 2 T05984 hypothetical 197 10.8 429 2 T31001 hypothetical 194 10.7 300 2 T25275 hypothetical 157.5 8.7 404 2 C95206 glycospit tran 157.5 8.7 546 2 G86221 hypothetical 147.5 8.1 442 2 A77433 hypothetical 147.5 7.9 321 2 T24773 hypothetical 140 > 7.7 470 2 A84772 hypothetical 134 7.4 376 2 T40488 hypothetical 135 7.3 398 2 G95205 glycospit tran 137 7.2 406 2 H95205 glycospit tran 138 7.3 398 2 G95205 glycospit tran 129.5 7.1 380 2 S55176 glycospit tran 110 6.1 491 2 S58330 probable memb	12	225.5	12.4		7	T40489	hypothetical prote	
205 11.3 33.2 T05984 hypothetical 197 10.8 429 2 T31001 hypothetical 194 10.7 300 2 T25275 hypothetical 197 10.8 429 2 T31001 hypothetical 197 2 S55490 hypothetical 157.5 8.7 404 2 C95206 hypothetical 157.5 8.7 546 2 G86221 hypothetical 147.5 8.1 44.2 A71433 hypothetical 143.5 7.9 321 2 T24773 hypothetical 140 7.7 470 2 A84772 hypothetical 132 7.3 398 2 G95205 glycosyl tran 131 7.2 406 2 H95205 glycosyl tran 129.5 7.1 380 2 S55176 GLG2 protein 110 6.1 286 2 S16423 hrobable members 110 6.1 491 2 S58330 hrobable members 110 6.1 491 2 S58330 hrobable members 120 120 120 120 120 120 120 120 120 120	13	205.5	11.3		7	A45729	qîycoqenin homolog	ò
197 10.8 429 2 T31001 hypothetical 194 10.7 300 2 T25275 hypothetical hypothetical 165 9.1 370 2 S55490 hypothetical hypothetical 157.5 8.7 404 2 C95206 hypothetical 157.5 8.7 546 2 G86221 hypothetical 147.5 7.9 321 2 T24773 hypothetical 140 7.7 470 2 A84772 hypothetical 134 7.4 376 2 T44048 hypothetical 134 7.3 398 2 G92205 glycosyl tran 131 7.2 406 2 H95205 glycosyl tran 129.5 7.1 380 2 S55176 GLG2 protein 110 6.1 286 2 S16423 probable members 110 6.1 491 2 S58330 probable members 120 110 6.1 491 2 S58330	14	205	11.3		7	T05984	hypothetical prote	•
194 10.7 300 2 T25275 hypothetical 165 9.1 371 2 S55490 hypothetical 157.5 8.7 404 2 C95206 glycosyl trans 157.5 8.7 546 2 G86221 hypothetical 147.5 8.7 546 2 A77433 hypothetical 147.5 7.9 321 2 T24773 hypothetical 143.5 7.9 321 2 T24773 hypothetical 140 > 7.7 470 2 A84772 hypothetical 134 7.4 376 2 T40488 hypothetical 134 7.4 376 2 T40488 hypothetical 135 7.3 398 2 G95205 glycosyl trans 138 7.3 380 2 G95205 glycosyl trans 159.5 7.1 380 2 S55176 flycosyl trans 110 6.1 286 2 S16423 probable members 110 6.1 491 2 S58330 probable members 110 6.1 491 2 S58330 probable members 110 6.1 491 2 S58330	15	197	10.8		7	T31001	hypothetical prote	qa
165 9.1 371 2 555490 hypothetical 157.5 8.7 404 2 C95206 glycosyl tran 157.5 8.7 546 2 G86221 protein F7G19 147.5 8.1 442 2 A71433 hypothetical 147.5 8.1 442 2 A71433 hypothetical 140° 7.7 470 2 A84772 hypothetical hypothetical 134 7.4 376 2 T40488 hypothetical 132 7.3 398 2 G95205 glycosyl tran 131 7.2 406 2 H92205 glycosyl tran 129.5 7.1 380 2 S55176 glycosyl tran 118 6.5 114 2 JC6077 pl 3 protein 110 6.1 491 2 S58330 probable members	16	194	10.7		~	T25275		
157.5 8.7 404 2 C95206 157.5 8.7 404 2 C95206 147.5 8.1 442 2 A71433 143.5 7.9 321 2 T24773 1340 7.7 470 2 A84772 134 7.3 398 2 G95205 131 7.2 406 2 H95205 129.5 7.1 380 2 S55176 118 6.5 114 2 JCC677 110 6.1 286 2 S16423 110 6.1 491 2 S58330	17	165	9.1	371	7	S55490	hypothetical prote	δò
157.5 8.7 546 2 G86221 147.5 8.1 44.2 2 A71433 143.5 7.9 321 2 T24773 140 ~ 7.7 470 2 A84772 134 7.4 376 2 T40488 132 7.3 398 2 G95205 131 7.2 406 2 H95205 129.5 7.1 380 2 S55176 110 6.1 286 2 S16423 110 6.1 491 2 S58330	18	157.5	8.7	404	7	C95206	qlycosyl transfera	•
147.5 8.1 442 2 A71133 143.5 7.9 321 2 T24773 134 7.4 376 2 T40488 132 7.3 406 2 F40488 131 7.2 406 2 F95205 129.5 7.1 380 2 S5576 110 6.1 286 2 S16423 110 6.1 491 2 S58330	19	157.5	8.7	546	7	G86221	protein F7G19.14 [qa
143.5 7.9 321 2 T24773 140 7.7 470 2 A84772 134 7.4 376 2 T40488 132 7.3 398 2 G95205 131 7.2 406 2 H95205 129.5 7.1 380 2 S55176 118 6.5 114 2 JCG077 110 6.1 286 2 S16423 110 6.1 491 2 S58330	20	147.5	8.1	442	7	A71433	hypothetical prote	
140	21	143.5		321	7	T24773	hypothetical prote	δ
134 7.4 376 2 740488 132 7.3 398 2 G95205 131 7.2 406 2 H95205 129.5 7.1 380 2 S55176 110 6.5 114 2 JC6077 110 6.1 491 2 S58330	22	140	•	470	7	A84772	probable glycogeni	•
132 7.3 398 2 G95205 131 7.2 406 2 H95205 129.5 7.1 380 2 S55176 118 6.5 114 2 JC6077 110 6.1 286 2 S16423 110 6.1 491 2 S58330	23	134	7.4	376	7	T40488	hypothetical prote	QC C
131 7.2 406 2 H95205 129.5 7.1 380 2 S55176 118 6.5 114 2 JC6077 110 6.1 286 2 S16423 110 6.1 491 2 S58330	24	132	7.3	398	7	G95205	glycosyl transfera	
129.5 7.1 380 2 S55176 118 6.5 114 2 JC6077 110 6.1 286 2 S16423 110 6.1 491 2 S58330	25	131	7.2	406	7	H95205	glycosyl transfera	δ
118 6.5 114 2 JC6077 110 6.1 286 2 S16423 110 6.1 491 2 S58330	26	129.5	7.1	380	7	S55176	GLG2 protein - yea	
110 6.1 286 2 \$16423 110 6.1 491 2 \$58330	27	118	6.5	114	7	JC6077	P13 protein - Leuc	qa
6.1 491 2 558330	28	110	6.1	286	7	S16423	general stress pro	
	29	110	6.1	491	7	558330	probable membrane	ا 0y

301 VVIGDSHKKQQTLQQFIEALSEAGALQYVKAPSAA 335

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lipopolysaccharide hypothetical prote	glycosyl transfera hypothetical prote	probable LPS biosy	probable remorane probatys	qenome polyprotein	hypothetical prote	hypothetical prote	hypothetical prote	lipopolysaccharide	lipopolysaccharide	hemocyanin chain e	dynein beta heavy	cobyrinic acid a,c
A71707 D95206	A95206 H91191	A86039	S49645	GNNY1B	T51525	T15067	AE2277	AH0972	S47847	BHTLE	T14914	D64477
2.2	010	210	10	Н	7	7	7	7	~	Н	~	7
517 696	814 335	335	1251	2157	572	175	311	337	338	624	4589	443
6.0	0.00 0.00	ر و و		5.7	5.6	5.4	5.4	5.3	5.3	5.3	5.2	5.5
108.5	108 107	107	105	103.5	101	97.5	97.5	96.5	96.5	96.5	92	94.5
30 31	33 33	34	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 Stocked and addition synthase F25P12.95 [imported] - Arabidopsis thaliana C:Species Arabidopsis thaliana (mouse-ear cress) C:Apecies Arabidopsis thaliana (mouse-ear cress) C:Apecies Arabidopsis thaliana (mouse-ear cress) C:Apecies (Arabidopsis thaliana) C:Apecies (Arabidopsis A.) Facker, J. William (A.) Fall, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon C:Apecies (A.) Facker, J. Ban, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon C:Apecies (A.) Fall, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Abauthors: Hunter, J.L.; Thinks, J. J. Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A.; Liu, J. H.; Lil, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Matil, R.; Marzia R:Apathors: Salabesy, T.; Rowley, D.; Sakan, S.; A.; Schanter, J.C.; Davis, R.W. A.; Wu, D.; Yu, G.; Fraser, C. M.; Venter, J.C.; Davis, R.W. A.; Wu, D.; Yu, G.; Fraser, C. M.; Venter, J.C.; Davis, R.W. A.; Accession: Gs66na A.; Accession: Gs61na A.; Accession: Gs66na A.; Access

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us-09-810-506-2.rpr

g

C; Accession: F86226

A; Map position: 1

61 22 121

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241

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WST76 protein - rice
C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Species: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T07610
R;Takahashi, R.; Joshee, N.; Kitagawa, Y.
Plant Mol. Biol. 26, 339-352, 1994
A;Title: Induction of chilling resistance by water stress, and cDNA sequence analysis A;Reference number: S52642; MUID:95036005
A;Reference number: S52642; MUID:95036005
A;Accession: T07610
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
                                          A;Cross-references: GB:AE002093; NID:g2275196; PIDN:AAB63818.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKMIYLDGDIQVYENIDHLFDLPDGYLYAVMDCFCEKTWSHTPQYKIRYCQQCPDKVQWP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 DIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                            NKMIYLDGDIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAKLGPKPPLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 VYNLVLAMLWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYN 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLVVAVLPDVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEFVEY 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:D26537; NID:g454879; PIDN:BAA05538.1; PID:g537404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                     1 MAPGLTQTADAMSTVTITKPSLPSVQDSDRAYVTFLAGNGDYVKGVVGLAKGLRKVKSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAPEI------NTKLTVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8;
                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                 Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 328;
                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 DESLDYKN-VVIGDSHKKQQTLQQFIEALSEAGALQYVKAPSAA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.6%; Score 1319; DB 2; 71.0%; Pred. No. 7.5e-102; ative 41; Mismatches 48;
                                                                                                                                                                                                 ; Score 1390.5; DB 2;
; Pred. No. 9.3e-108;
31; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain Somewake
                                                                                                                                                                                                   76.6%;
ilarity 74.7%;
Conservative 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Note: induced by water stress
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                                                                                                                                                                                                                        Best Local Similarity
Matches 257; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-328 <TAK>
                          1-344 <STO>
A; Molecule type: DNA
                                                                                                 A;Gene: At2947180
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238;
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                                                                                                                                                                                                        Query Match
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                          A; Residues:
                                                                            C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                          23
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Mature 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.Rocession: F86226
A.Accession: PRe226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB: AE005172; NID: 93482910; PIDN: AAC33195.1; GSPDB: GN00141 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84912
                                                                                                                                                 hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAPEINTKLTVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAPEMNNKLSY-----GEKKRAYVTFLAGTGDYVKGVVGLAKGLRKTKSKYPLVVAVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 PLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable galactinol synthase [imported] - Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.5%; Score 1516.5; DB 2
80.9%; Pred. No. 3.1e-118;
  30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 275; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-334 <STO>
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C; Accession: T02295
R; Vysotskala, V.S.; Schwartz, J.R.; Kwan, A.; Toriumi, M.; Yu, G.; Oji, O.; Liu, S.; rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel submitted to the EMBL Data Library, June 1998
A; Description: Arabidopsis thaliana chromosome 1 BAC T13D8 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AC004473; NID:g3108025; PID:g3249091; GSPDB:GN00059; ATSP:T1
                      R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, March 1999
                                                                                                                                                                                                                                                                                                                                                                                                         2
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----FVEYNKM 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 IYLDGDIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 KRAYVIFLAGIGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 KRAYVTFLAGNKDYWAGVVGLAKGLRKVKSAYPLVVAILPDVPEEHRQILLAQGCIIREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGPKPPLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVLAMLWRHPENIELDOVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDES
                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 345;
                                                                                                                                                               A;Cross-references: EMBL:AL049171; GSPDB:GN00062; ATSP:T25K17.60
A;Experimental source: cultivar Columbia; BAC clone T25K17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                         61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 LDYKNVVIGDSHKKQQTLQQFIEALSEAGALQYVKAPSAA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.1%; Score 1110; DB 2; 59.9%; Pred. No. 1.8e-84;
                                                                                                                                                                                                                                                                                                                                                                                 ; Pred. No. 8.6e-92
31; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                          66.0%; Score 1198.5; 65.0%; Pred. No. 8.6e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 EPVYPPENQTEFAMAYYVINYSKLRIWE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: translated from GB/EMBL/DDBJA; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                       Matches 221; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                             A; Map position: 4
A; Introns: 136/3; 244/3; 289/3
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A;Introns: 119/3; 227/3; 272/3
                                                                       A; Reference number: 215382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: 214649
                                                                                                                   A; Molecule type: DNA
A; Residues: 1-361 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                       A; Gene: ATSP: T25K17.60
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C; Accession: T06009
                                                                                               T06009
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Best Local
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Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Titles: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719
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                                                                                                                                                                                                                                                                                                                                                     C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: H96629
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 22-Oct-1999
58 VLPDVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIY 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                    LWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLDYKN
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                                                                                                                                                                                                                                                                                                                               hypothetical protein F8A5.2 [imported] - Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.5%; Score 1298.5; DB 2
70.7%; Pred. No. 3.9e-100;
ive 35; Mismatches 52;
                                                                                                                                                             301 VVIGDSHKKQQTLQQFIEALSEAGALQYVKAPSAA 335
                                                                                                                                                                                          Best Local Similarity 70.77
Matches 241; Conservative
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A;Molecule type: DNA
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glycogenin glucosyltransferase (EC 2.4.1.186) - human
N.Alternate names: glycogen(starch) synthase, glycogenin subunit
N.Contains: glycogen(starch) synthase, glycogenin subunit
C.Species: Homo sapiens (man)
C.Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 11-Jun-1999
C.Accession: JC4695; G01948; S45141
R.Barbetti, F.; Rocchi, M.; Bossolasco, M.; Cordera, R.; Sbraccia, P.; Finelli, P.; C
Biochem. Biophys. Res. Commun. 220, 72-77, 1996
A; Fitle: The human skeletal muscle glycogenin gene: cDNA, tissue expression, and chro
A; Recession: JC4695; MUID:96176958
A; Accession: JC4695
A; Molecule type: mRNA
A; Residues: 1-333 < ABREA
A; Residues: 1-333 < A
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A) Pathway: glycogen/starch biosynthesis
A) Note: required to initiate the synthesis of glycogen
C; Superfamily: glycogenin
C; Superfamily: glycogenin
C; Keywords: acetylated amino end; glycogen/starch biosynthesis; glycoprotein; glycosy
F; 2/Modified site: acetylated amino end (Phr) (in mature form) #status predicted
F; 195/Binding site: carbohydrate (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-203, 'KMSQEPYHICPLGRSQLWHSRLYPRKNGR','NDGNRARLIIWEQIPLITSRGNLTLISSR','NT
A; Cross-references: EMBL:X79537; NID:g496894; PIDN:CAA56073.1; PID:g496895
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on a specific tyrosine res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL:U31525; NID:9976399; PIDN:AAB09752.1; PID:9976400 R; Leffers, H.; Wiemann, S.; Ansorge, W. R. Leffers do the EMBL Data Library, June 1994 A; Description: Cloning and sequencing of a cDNA encoding human glycogenin. A; Reference number: $45140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 IEPVYPPENQTEFAMAYYVINYSKIRIWEFVEXNKMIYLDGDIQVFDNIDHLFDLPNGQF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 YAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYH 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 NLLETVKIVPPTLFAEQDFLNMYFK-----DIYKPIPPVYNLVLAMLWRHPENIEL--DQ 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 QLLHLASEQGSFDGGDGILNTFFSSWATTDIRKHLPFINLSSISISSYLPAFKVFGAS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 AKVVHFLGR-VKPWNYTYDPKTKSVKSEAHDPNWTHPEFLIL---WWNIFTTNVL---- 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 VKVVHYCAAGAKPWRFT------GEEENMDREDIKMLVKKWWDIYNDESLDYKNV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB:U44131; NID:g1174166; PIDN:AAB00114.1; PID:g1174167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 333;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: catalyzes the alpha-glucosylation of itself
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Experimental source: skeletal muscle
R;Rodriguez, I.R.
submitted to the EMBL Data Library, July 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: G08914
A; Accession: G01948
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Matches 78; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-333 <ROD>
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JC4695
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A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1201 <FED>
A; Cross-references: EMBL: AC004260; NID: 93176694; PID: 93540195; GSPDB: GN00059; ATSP: T14N5
A; Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T14N5.1 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Cispecies: Arabidopsis thaliana (mouse-ear cress) (Cispecies: O1-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 22-Oct-1999 (Ciscossion: T00444 R;Federspiel, N.A.; Palm, C.J.; Conway, A.B.; Kurtz, D.B.; Conway, A.R.; Au, M.; Araujo, yysotskala, V.S.; Yu, G.; Ecker, J.; Theologis, A.; Davis, R.W. submitted to the EMBL Data Library, September 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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-EFVEYNKMIYL 118
                                       DGDIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGP 178
                                                                                                                                                                               190 PPSPYFNAGMFVFEPNPLTYESLLQTLQVTPPTPFAEQDFLNMFFGKVFKPVSPVYNLIL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                836 QLRQKLQLPVGSCELSVPLQAKDNFYSAGAKKEAYATILHSAQFYVCGAIAAAQSIRMSG 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKYPLVVAVLPDVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEF 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 VEYNKMIYLDGDIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKV 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAK 49
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                                                                                                                                                                                                                                                                           179 KPPLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 KPKSPAD---LEATVLESTIIASVTEAPLSYSPAAPSAA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 KNVVIGDSHKKQQTLQQ--FIEALSEAGALQYVKAPSAA 335
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Best Local Simi
Matches 85;
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Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hudhes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A;Authors: Hunter, J.L.; Jankins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.H.; Li, T.H.; Li, Y.; Lin, X.; Liu, S.A.; Luros, J.S.; Maiti, E.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome I of the plant Arabidopsis.
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**R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A submitted to the EMBL Data Library, February 1998
A;Reference number: 221910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-557 <STO>
A;Cross-references: GB:AE005173; NID:g9857520; PIDN:AAG00875.1; GSPDB:GN00141
                                                                                                                                                           hypothetical protein T24C10.6 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 ENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDLPNGQFYAVMDCF 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : || :|| | | | | | ::
222 PRLKQKLLMPVGSCQIAPSFAQFGQEAWRPKHEDNLASKAVTALPRRLRVAYVTVLHSSE 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96; Indels 134; Gaps
263 FGLVQDTCSYQHVEDVSGAVSHLSLGETPATTQPFVSSEERKERWEQGQADYMGADS 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----AYVTFLAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 DYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDH---RKQLVD---QGCVVKEIEPVYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 CEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYHNLLETVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 PENIELDQVKVVHYCAAGAKPW-RFTGEEENMDREDIKMLV----KKWWDIYNDESLDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               416 KIESYNGGDQGFLNEIF-------WWHRLSKRVNTMKYFDEKNHRRHDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336 FSQKD---SYNEWNYSKLRVWQVTDYDKLVFIDADFIILKKLDHLF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.8%; Score 232; DB 2; 21.6%; Pred. No. 2.6e-11; tive 53; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 IVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAMLWRH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PEINTKLTVPVHS-----ATGGEKR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 78; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                 C; Accession: H96590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: T24C10.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 K 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     512 K 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
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A; Accession: A45094
A; Molecule type: mRNA
A; Residues: 1-32 < VIS>
A; Note: sequence extracted from NCBI backbone (NCBIP:120846)
B; Campbell, D.G; Cohen, P. Surfite: The amino acid sequence of rabbit skeletal muscle glycogenin.
A; Reference number: S06482; MUID:9003266
A; Accession: S06482; MUID:9003266
A; Accession: S06482
A; Reference number: S06482; MUID:9003266
A; Residues: 1-87, S; May Pa, Protein
A; Residues: 1-87, S; May Pa, Protein
A; Residues: 1-87, S; May Pa, Protein
A; Reference number: S02470
A; Title: Identification of the 38-kma subunit of rabbit skeletal muscle glycogen synthas A; Accession: S02470
A; Title: Identification of the 38-kma subunit of rabbit skeletal muscle glycogen synthas A; Residues: 9-19; 38-44, M' 90-94; 204-207, F', 209-210, KH', 213-219 cprT>
C; Function: A; Pycogen fararch biosynthesis of glycogen and UDP
A; Residues: 9-19; 38-44, M', 90-94; 204-207, F', 209-210, KH', 213-219 cprT>
C; Function: C; Reyards fararch biosynthesis of glycogen acceptated maino end glyr) # status experimental
C; Superfamily: glycogenin one of glyrogen/status protein plosynthesis; glycoprotein; glycosyltr F; 1/Modified site: cactylated amino end (Trr) fstatus experimental
F; 194/Binding site: carbohydrate (Tyr) (covalent) # status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                       ξn
                                                                                                                                                                                       glycogenin glucosyltransferase (EC 2.4.1.186) - rabbit
N;Alternate names: glycogen synthase 38K chain; glycogenin
C;Species: Orytolagus cuniculus (domestic rabbit)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 11-Jun-1999
C;Accession: A45094; S06482; S02470
R;Viskupic, E.; Cao, Y.; Zhang, W.; Cheng, C.; DePaoli-Roach, A.A.; Roach, P.J.
J. Biol. Chem. 267, 25759-25763, 1992
A;Title: Rabbit skeletal muscle glycogenin. Molecular cloning and production of fully A;Reference number: A45094; MUID:93100288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 YAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYH 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 QLLHVASEQGSFDGGDQGLLNTFFNSWATTDIRKHLPFIYNLSSISIYSYLPAFKAFGAN 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----DESLDYKNV--VIGD-SH-----KKQQTLQQFIEALS-----EAGALQYVKAPS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 VKVVHYCAAGAKPWRFT------GEEENMDREDIKMLVKKWWDIYN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.0%; Score 235.5; DB 1; Length 3 23.8%; Pred. No. 6.9e-12; tive 49; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 13.0%
Best Local Similarity 23.8%
Matches 85; Conservative
                            ------PLLQOF 264
                        259
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hypothetical protein F17M5.90 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr.1999 #sequence_revision 30-Apr.1999 #text_change 22-Oct-1999
C;Accession: T05984 M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer,
submitted to the Protein Sequence Database, March 1999
A;Reference number: 215263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 29-Oct-1999
C.Accession: T31001
A.Description: The sequence of C. elegans cosmid F56B6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 NLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAMLW-----RHPEN----IE 249
                                                                                |:| |: || :| |: |: : | | :| :| || :| || :| || :| || :| || 145 GVFTARPSTDTYARMLEALDV--PGAFWRRTDQSFLQQFFDD-WQGLPVFCNMLQYVWFA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 IEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDLPNGQF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 YAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYH 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :: || || : || || : || : || :: || |:: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || ::
                                 187 GMFVYEPNLSTYHNLLETVKIVPPTLF---AEQDFLNMYFKDIYKPIPPVYNLVLAMLWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 LDQVKVVHYCAAGAKPW-----RFTGEEENMDREDIKMLVKKWWDIYNDESLD 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-313 <BEV>
A; Cross-references: EMBL:AL035678; GSPDB:GN00062; ATSP:F17M5.90
A; Experimental source: cultivar Columbia; BAC clone F17M5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                         244 HPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.3%; Score 205; DB 2; Lk
23.6%; Pred. No. 2.4e-09;
tive 50; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F56B6.4 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-429 <STE> A;Residues: 1-629 <STE> A;Cross-references: EMBL:064599; PIDN:AAB04562.1 A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 ---MSATGNDVW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: ATSP:F17M5.90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: T05984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 4
A; Introns: 193/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pp
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C;Species: Rhodobacter sphaeroides
C;Species: Rhodobacter sphaeroides
C;Accession: A45729, 4*sequence_revision 03-May-1994 #text_change 08-oct-1999
C;Accession: A45729, 237663
R;Benning, C; Somerville, C.R.
A; Dacteriol. 174, 6479-6487, 1992
A;Tille: Identification of an operon involved in sulfolipid biosynthesis in Rhodobacter
A;Reference number: A45729, MuID:93015699
A;Accession: A45729
A;Accession: A45729
A;Accession: A45729
A;Accession: A45729
A;Accession: A45729
A;Accession: A45729
A;Accession: Calculation
C;Genetics: 1-260 <BEN>
A;Accession: Calculation
A;Accession
A;Accessi
                                     A; Molecule type: DNA
Msesidues: 1-37 2 KMO2
A; Residues: 1-37 2 KMO2
A; Cross-references: EMBL: AL021730; PIDN: CAA16830.1; GSPDB: GN00067; SPDB: SPBC4C3.08
A; Experimental source: strain 972h-; cosmid c4C3
A; Genetics:
A; Genetics: SPBB: SPBC4C3.08
A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 HAREALHARAAFTKGGKPPFHTPLDNFAKLRLWQLVDYRSVVFIDADALVLRNVDRLFDY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 PNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLY-----FNA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 VKFKPTKSKYPVVVLAMKGIDQMKLDQLQEDGAIVKVVDPLYAHEVVDDVNDIALLDSRW 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 CFCEKTWSHSPQYKIGYCQQCP-----DKVTWPEAKLGPKPPL--YFNAGMFVYEPNL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 IFWRRFTEEFAAYGLTRDDLYPYVFAAVSDPGMWHET----PPPFKDYFNAGLFVFKPLK 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 AHYKRLMALARF--PKLYDNANMMEQSLLNF------AYNSAGAFPWESLDWTFN 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----AAPNVYESLSDFHRMNS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- PNGOFYAV-MD 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 EFAMAYY------VINYSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDL 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 RK----AKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKEIEPVYPPE-----NQTEFAMAYY 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 DYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKEIE--PVYPPENQT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 APEINTKLTVPVHSATG---GEKRAYVTFL---AGTGD------YVKGVVGLAKGL 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 SPEIQRS----VYTLTGLAPSSKMAFVTMLTVRAANGENEVENTQQDWYYNSTRLLVHRL 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STYHNLLETVKIVPPTLF----AEQDFLNMYFKDIYKPIPPVYNLVLAMLWRH-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 ---PENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYND 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 225.5; DB 2;
; Pred. No. 5.4e-11;
44; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.3%; Score 205.5; DB 2 23.2%; Pred. No. 1.6e-09;
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 VINYSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.4%; 25.3%;
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Best Local Similarity 25.3%
Matches 89; Conservative
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Best Local Similarity
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Gaps

us-09-810-506-2.rpr

A;Introns: 41/3; 105/3; 146/1; 202/2; 245/3; 371/3; 390/3 A;Note: F56B6.4

16; 62 VENSNDSDNLRLIERPDLGVFFTKLHCWRLTQYTKCVFLDADTLVLRNADELFTRPD--F 119 120 SAASD------FUSGVFYYVPNNETYR 146 200 NLLETVKIVPPTLFA------EQDFLNMYF---KDIYKP--IPPVYNLVLAMLW--- 242 83 VYPPENQTEFAMAY --- YVINYSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDLPNGQF 139 140 YAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYH 199 243 ----RHPENIELDQVKVVHYCAAGAKPWR-----FTGEEENMDREDIKMLVKKWWDIY-- 291 Gaps 23 AYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKEIEP 82 :96 Length 429; Query Match 10.8%; Score 197; DB 2; Length 429 Best Local Similarity 23.6%; Pred. No. 1.5e-08; Matches 75; Conservative 46; Mismatches 101; Indels 241 HVNHTSRTNEHAAVFPSH 258 292 -- NDESLDYKNVVIGDSH 307 δ ζζ Op qq Db Qy qq οy

Search completed: July 2, 2002, 12:09:34 Job time: 181 sec

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July 2, 2002, 12:08:56; Search time 23.19 Seconds (without alignments) 352.849 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                             rotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                     231628 seqs, 24425594 residues
                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                        Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1816
                                                                                                                                                                                                                                                                                                                   BLOSUM62
                                                                                                                                                                                                                                                 Perfect score:
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Issued_Patents_AA:* Database :

Maximum Match 100% Listing first 45 summaries

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8 90 5.0 372 1 US-08-753-233-3 Sequence 3, 0 90 5.0 372 2 US-08-948-246-3 Sequence 3, 1 89.5 4.9 354 1 US-08-753-233-2 Sequence 2, 2 89.5 4.9 354 2 US-08-948-246-2 Sequence 2, 3 89.5 4.9 354 2 US-08-948-246-2 Sequence 2, 4 88 4.8 71 4 US-09-149-674-2 Sequence 2, 5 87 4.8 510 2 US-08-557-122A-3 Sequence 10, 6 87 4.8 510 4 US-09-266-36 Sequence 36, 7 4.8 510 4 US-09-266-36 Sequence 36, 87 4.8 510 4 US-09-266-36 Sequence 36, 87 4.8 593 5 PCT-0533-07923-1 Sequence 11,	17	108.5	0.9	674	4	-08-961-083-	200,
9 90 5.0 372 2 US-08-984.246-3 Sequence 3, 0 5.0 372 2 US-08-149-674-3 Sequence 3, 0 5.0 5.0 372 2 US-09-149-674-3 Sequence 3, 0 5.0 5.0 374 2 US-09-149-674-2 Sequence 2, 0 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5	18	06	•	372	П	3-753-233	3,
0 90 5.0 372 2 US-09-149-674-3 Sequence 3, 289.5 4.9 354 1 US-08-553-233-2 Sequence 2, 289.5 4.9 354 2 US-08-984-246-2 Sequence 2, 3, 289.5 4.9 354 2 US-09-149-674-2 Sequence 2, 4 88 4.8 71 4 US-09-073-297-10 Sequence 10, 289.5 4.8 510 2 US-09-255-122A-36 Sequence 10, 289.5 4.8 510 2 US-08-557-122A-36 Sequence 36, 287 4.8 510 4 US-09-265-666-36, 36 Sequence 36, 289.5 5 PCT-US93-07923-11 Sequence 11, 289.5 5 US-08-259-07923-11 Sequence 11, 289.5 5 US-08-259-07923-11	19	90	•	372	7	-08-984-246	ς,
1 89.5 4.9 354 1 US-08-753-233-2 Sequence 2, 3 89.5 4.9 354 2 US-08-944-246-2 Sequence 2, 3 89.5 4.9 354 2 US-09-149-674-2 Sequence 2, 4 88 4.8 7.1 4 US-09-073-297-10 Sequence 10, 5 87 4.8 510 2 US-08-557-122A-36 Sequence 36, 6 87 4.8 510 4 US-09-265-666-36 Sequence 36, 7 4.8 593 5 PCT-US93-07923-11 Sequence 11,	20	σ	•	372	7	-09-149-674	3,
2 89.5 4.9 354 2 US-08-984-246-2 Sequence 2, 3 89.5 4.9 354 2 US-09-149-674-2 Sequence 2, 4 88 4.8 71 4 US-09-073-297-10 Sequence 36, 87 4.8 510 2 US-08-557-122A-36 Sequence 36, 87 4.8 510 4 US-09-262-666-36 Sequence 36, 87 4.8 593 5 PCT-US93-07923-11 Sequence 11,	21	9	•	354	7	-08-753-233	7
3 89.5 4.9 354 2 US-09-149-674-2 Sequence 2, 4.8 71 4 US-09-073-297-10 Sequence 10, 5 87 4.8 510 2 US-08-557-1228-36 Sequence 36, 87 4.8 510 4 US-09-262-666-36 Sequence 36, 87 4.8 593 5 PCT-US93-07923-11 Sequence 11,	22	9	4.9	354	7	-08-984-246	7
4 88 4.8 71 4 US-09-073-297-10 Sequence 10, 5 87 4.8 510 2 US-08-257-122A-36 Sequence 36, 6 87 4.8 510 4 US-09-265-36 Sequence 36, 7 87 4.8 593 5 PCT-US93-07923-11 Sequence 11,		σ	4.9	354	7	-09-149-674	7
87 4.8 510 2 US-08-557-122A-36 Sequence 36, 87 4.8 510 4 US-09-262-666-36 Sequence 36, 87 4.8 593 5 PCT-US93-07923-11 Sequence 11,		88	4.8	71	4	-09-073-2	10,
87 4.8 510 4 US-09-262-666-36 Sequence 36, 87 4.8 593 5 PCT-US93-07923-11 Sequence 11,	25	87	4.8	510	~	-08-557-122A-	36,
3 5 PCT-US93-07923-11 Sequence 11,	56	87	4.8	510	4	US-09-262-666-36	36,
	27	87	4.8	593	ഹ	-US93-07923	11,

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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
PCT-US93-07923-2	US-08-230-491A-3	US-08-619-280A-3	US-08-940-391-3	US-09-794-236-1	US-08-750-532-1	US-08-750-532-9	US-08-894-818B-8	US-09-445-472-6	US-09-356-952-4	US-08-738-168B-5	PCT-US93-07923-3	US-07-966-278-1	US-08-424-921-1	US-08-556-355A-1	US-07-803-627A-1	US-08-688-649-37	US-08-557-122A-28
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759	992	997	166	166	903	1398	1398	1398	1589	521	755	775	775	775	775	176	510
4.8	4.8	4.8	4.8	4.8	4.7	4.7	4.7	4.7	4.7	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5
87	87	87	87	87	85	85	85	82	82	82.5	82.5	82.5	82.5	82.5	82.5	۵.	82
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPOTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
                                                                                         APPLICANT: LIGHTNER, JONATHAN EDWARD
TITLE OF INVENTION: STARCH BIOSYNTHETIC ENZYMES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/852615
FILING DATE: MXY 7, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: 41,173
REFERNEX/COCKET NUMBER: BB-1083-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
US-09-073-297-6
; Sequence 6, Application US/09073297
; Patent No. 6255114
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: not relevant TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-09-073-297-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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Length 328; Query Match 72.6%; Score 1319; DB 4; Best Local Similarity 71.0%; Pred. No. 1.2e-138; Matches 238; Conservative 41; Mismatches 48;

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                                                          58 DVPGEHRRKLVEGGCVVREIQPVYPPESQTQFAMAYYVINYSKLRIWEFVEYERMYYLDA 117
                                                                                                                    DIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKP 180
                                                                                                                                         PLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAM 240
                                                                                                                                                                                                                          241 LWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLDYKN 300
                                                                                                                                                                                                                                                                                                     69; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 KRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKEI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 REAYATILHSASEYVCGAITAAQSIRQAGSTRDLVILVDDTISDHHRKGLESAGWKVRII 66
2 MGPNVSSE----KKALAAAKRRAYVTFLAGDGDYWKGVVGLAKGLRRVRSAYPLVVAVLP 57
                                       61 DVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDG
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STREET: 1007 MARKET STREET
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14.6%; Score 265.5; DB 4;
Best Local Similarity 27.6%; Pred. No. 3.6e-21;
Matches 81; Conservative 45; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09073297
Patent No. 6255114
GENERAL INFORMATION:
APPLICANT: LIGHTNER, JONATHAN EDWARD
TITLE OF INVERTION: STARCH BIOSYNTHETIC ENZYMES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                             301 VVIGDSHKKQQTLQQFIEALSEAGALQYVKAPSAA 335
                                                                                                                                                                                                                                                                                                                                                                                 298 ----EEDNADEASQPMRTALAEAGAVKYFPAPSAA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: MICROSOFT WINDOWS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: MICROSOFT WORD VERSION 7.0A CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/073,297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/852615
FILING DATE: MAY 7, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1083-B
TELEPHONE: 302-992-4926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: DISKETTE, 3.50 INCH
IBM PC COMPATIBLE
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                     SERINDKAERD---AYNEWNYSKFREWQLIDYDKVIFIDADLLILERNIDFLFALP---- 118
                                                                                                                                                                                                    147 LMEHIDEITSYNGGDQGYLNEIFTWWHR-IPKHMNF-LKHFWEGDE----EEVKAKKTRL 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDLPNGQFY 140
                                                                                141 AVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYHN 200
                                                                                                                       --ATGNNATL-----FNSGVMVIEPSNCTFRL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43; Mismatches 120; Indels 74; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 RAYVIFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQL--VDQGCVVKE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 QAFVT-LTTNDAYAKGALVLGSSLKQHRTTRRLVVLATPQVSDSMRKVLETVFDEVIMVD 62
                                                                                                                                                                 201 LLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAMLWRHPENIELDQVK----
                                                                                                                                                                                                                                                 255 ------VVHYCAAGAKPWR-FTGEEENMDREDIKMLVK-----KWWDIYN 292
                                                                                                                                                                                                                                                                            201 FGANPPVLYVLHY--LGRKPWLCFRDYDCNWNVEILREFASDVAHARWWKVHN 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: E. I. DU PONT DE NEMOURS AND COMPANY 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LIGHTNER, JONATHAN EDWARD TITLE OF INVENTION: STARCH BIOSYNTHETIC ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 241; DB 4;
Pred. No. 1.9e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BB-1083-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/073,297 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/852615
FILING DATE: MAY 7, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09073297
Patent No. 6255114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MAJARIAN, WILLIAM R. REGISTRATION NUMBER: 41,173 REFERENCE/DOCKET NUMBER: BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 333 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Best Local Similarity
Matches 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: LIGHTNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DELAWARE
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                                                                                                                          119 -----EIT--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         us-09-073-297-3
                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-09-073-297-3
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453 KYFGDESRHDKARNLPENLE----GIHY--LGLKPWRCYRDYDCNWDLKTRRVYASESV 505
135 PNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPN 194
                                                                   ------SYPQLSAAGNNKVLFNSGVMVLEPS 410
                                                                                                                                                                                                      ----VWWHRLSKRLNTM 452
                                                                                                                                                                                                                                                                          ----PENIELDQVKVVHYCAAGAKPWR-FTGEEENMDREDIKMLVK--- 285
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                                                                                                                                      195 LSTYHNL-LETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAMLWRH-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET CITY: WILMINGTON STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LIGHTNER, JONATHAN EDWARD
TITLE OF INVENTION: STARCH BIOSYNTHETIC ENZYMES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MICROSOFT WINDOWS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: MICROSOFT WORD VERSION 7.0A CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/073,297
                                                                                                                                                                                                   411 ACLFEDLMLKSFKIGSYN-GGDQGFLNEYF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/852615
FILING DATE: MAY 7, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: 41,173
REFERENCE/COCKET NUMBER: BB-1083-B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-073-297-14; Sequence 14, Application US/09073297; Patent No. 6255114; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14:
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Matches 44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , CLONE: rl0n.pk0027.fl1
US-09-073-297-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DVPEDHRKQLVDQG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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506 HARWWKVYD 514
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                                          140 YAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYH 199
                                                                                                                                   200 NLLETVKIVPPTLFAEQDFLNMYFK-----DIYKPIPPVYNLVLAMLWRHPENIEL--DQ 252
                                                                                                                                                                                 148 QLLHLASEQGSFDGGDGILNTFFSSWATTDIRKHLPFIYNLSSISISYLPAFKVFGAS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 CVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDL 134
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                                                                                                                                                                                                                                                                          -----GEEENMDREDIKMLVKKWWDIYNDESLDYKNV 301
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STATE: DELAGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LIGHTNER, JONATHAN EDWARD
TITLE OF INVENTION: STARCH BIOSYNTHETIC ENZYMES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19898

MONDPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IRM PC COMPATIBLE
SOFTWARE: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1083-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-426
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/073, 297
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/852615
FILING DATE: MAY 7, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09073297
Patent No. 6255114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           not relevant
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 566 amino acids
                                                                                                                                                                                                                                                                  253 VKVVHYCAAGAKPWRFT----
                                                                                                                                                                                                                                                                                                                                                                                                         302 VIGDSHKKQQTLQQF 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 -----PLLQQF 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: DELAWARE COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 FNSNDSENLSLIGRPDLGVTFTKFHCWRLTQYSKAVFLDADTMIIRNSDELFERPD--FS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 AVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYHN 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 AYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQ--GCVVKEI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 AWIT-LATNDRYAQGALTLLNSLHASGTTRRIHCLITNEISNSVREKLVNKFDEVTVVDI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.7%; Score 194; DB 4; Length 300; 22.6%; Pred. No. 2.7e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47; Mismatches 113; Indels
                                                                                                                                                                                                                                                                    ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET CITY: WILMINGTON STATE: DELAWARE
                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: LIGHTNER, JONATHAN EDWARD
TITLE OF INVENTION: STARCH BIOSYNTHETIC ENZYMES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET UMBER: BB-1083-B
TELECOMMUNICATION: 302-992-4926
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: DISKETTE, 3.50 INCH COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: MICROSOFT WINDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 KIVHFIGA-QKPWNSPPSDSGLHKNE 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 KVVHYCAAGAKPWRFTGEEENMDRED 279
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APPLICATION NUMBER: 08/852615
FILING DATE: MAY 7, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                               Sequence 4, Application US/09073297 Patent No. 6255114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
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Matches 60; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
111 : 11::11:11
58 DVPGEHRRKLVEOG 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                      US-09-073-297-4
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                                                                                                                                                                                           ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 IVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAMLWRHPEN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VTDPTPFAEQDFLNMFFRDVKRIPPVYNLVLAMLWRNPRN 43
                                                                                                      APPLICANT: LIGHTNER, JONATHAN EDWARD TITLE OF INVENTION: STARCH BIOSYNTHETIC ENZYMES NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/09073297
Patent No. 6255114
GENERAL INFORMATION: APPLICANT: LIGHTNER, JONATHAN EDWARD
TITLE OF INVENTION: STARCH BIOSYNTHETIC ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.3%; Score 187; DB 4; 78.0%; Pred. No. 8.3e-14; tive 5; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: MICROSOFT WINDOWS 95
MICROSOFT WORD VERSION 7.0A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE.
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
TYPE: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1083-B
                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,297
                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
RESULT 7
US-09-073-297-20
Sequence 20, Application US/09073297
Patent No. 6255114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/852615
FILING DATE: MAY 7, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 amino acids
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Best Local Similarity 78.0°
Matches 32; Conservative
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MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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SOFTWARE: MICROSO
                                                                                                                                                                                                                                        WILMINGTON
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                                                                                                                                                                                                                                                              STATE: DELAWARE
                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  U.S.A.
                                                                                                                                                                                                                                                                                                    19898
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                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
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; MOLECULE TYPE: protein US-08-312-387B-4
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 DNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----FN 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: DOT MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
ZID: A S. A
ZID: A S. A
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APPLICANT: LICHTNER, JONATHAN EDWARD
TITLE OF INVENTION: STARCH BIOSYNTHETIC ENZYMES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 AGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYF 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,297
OPERATING SYSTEM: MICROSOFT WINDOWS 95
              SOFTWARE: MICROSOFT WORD VERSION 7.0A CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/073,297
                                                                   FILING DATE:

CLASSIFTCATION:

PRIOR APPLICATION:

APPLICATION DATA:

APPLICATION NUMBER: 08/852615

FILING DATE: MAY 7, 1997

ATTORNEY AGENT INFORMATION:

NAME: MAJARIAN, WILLIAM R.

REGISTRATION NUMBER: 41, 173

REFERENCE/DOCKET NUMBER: BB-1083-B

TELECOMMUNICATION:

TELEPHONE: 302-992-4926

TELEFAX: 302-773-0164
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MEDIUM TYPE: DISKETTE, 3.50 INCH
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/852615
FILING DATE: MAY 7, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 27.28
                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide IMMEDIATE SOURCE:
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US-09-073-297-16
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US-09-073-297-12
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21 KRAYVIFLAGIGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKEI 80
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TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
UNMER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.0%; Score 145.5; DB 4; Length 93; Best Local Similarity 34.0%; Pred. No. 1.2e-08; Matches 32; Conservative 19; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Datentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,387B
FILING DATE: US/08/312,387B
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 EPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1083-B
TELECOMMUNICATION:
TELEPHONE: 302-992-4926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Jackson Eq., David A.
REGISTATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08312387B Patent No. 5545553 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION TELEPHONE: 201 487-5800
                                                                                                                           TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                                                                                                                                                                                                                                                           not relevant
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                                                                                                                                                                                                                                                                                                                                                          ; CLONE: ctaln.pk0013.e6 US-09-073-297-12
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: not rele
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
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80 ITTYARLKLGEYIADCDKVLYLDTDVLVRDGLKPLWDTDLGGNWVGACIDLFVER---- 134
                                                155 PQYKIGYCQQCPDKVTWPEAKLG-PKPPLYFNAGMFVYEPNLSTYHNL-----LETVK 206
                                                                                   135 ---QEGYKQ------KIGMADGEYYFNAGVLLINLKKWRRHDIFKMSCEWVEQYK 180
                                                                                                                                         207 IVPPTLFAEQDFLNMYFK-----DIYKPIPPVYNLVL-AMLWRHPENIELDQ----- 252
                                                                                                                                                                                   181 DV--MOYODODILNGLFKGGVCYANSRFNFMPTNYAFMANGFASRHTDPLYLDRTNTAMP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 PQYKIGYCQQCPDKVTWPEAKLG-PKPPLYFNAGMFVYEPNLSTYHNL-----LETVK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 ---QEGYKQ------KIGMADGEYYFNAGVLLINLKKWRRHDIFKMSCEWVEQYK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 VINYSKLRIWEFV-EYNKMIYLDGDIQVFDNIDHLFDLPNGQFY--AVMDCFCEKTWSHS 154
                                                                                                                                                                                                                                                             253 VKVVHYCAAGAKPW------RFT---GEEENMDRE-----DIKMLVKKW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GOLSCHLICH, EMIL C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.4%; Score 134; DB 1; Length 306; 25.0%; Pred. No. 1.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08683458 Patent No. 5798233 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-683-458-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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TELEFAX: 133521
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                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-08-683-458-4
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                                                                                        98 VINYSKLRIWEFV-EYNKMIYLDGDIQVFDNIDHLFDLPNGQFY--AVMDCFCEKTWSHS 154
                                                                                                                    155 PQYKIGYCQQCPDKVTWPEAKLG-PKPPLYFNAGMFVYEPNLSTYHNL-----LETVK 206
                                                                                                                                                                                                                             135 ---QEGYKQ------KIGMADGEYYFNAGVLLINLKKWRRHDIFKMSCEWVEQYK 180
                                                                                                                                                                                                                                                                      207 IVPPTLFAEQDFLNMYFK-----DIYKPIPPVYNLVL-AMLWRHPENIELDQ----- 252
                                                                                                                                                                                                                                                                                                                   181 DV--MOYODODILNGLFKGGVCYANSRFNFMPTNYAFMANGFASRHTDPLYLDRTNTAMP 238
                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             253 VKVVHYCAAGAKPW------RFT---GEEENMDRE------DIKMLVKKW 287
                                                   68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GOLSCALICA, EMIL C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
UNMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68;
    Length 306;
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                                              71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,426
Query Match
7.4%; Score 134; DB 1;
Best Local Similarity 25.0%; Pred. No. 1.4e-06;
Matches 59; Conservative 38; Mismatches 71;
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095B
TELECOMBUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New TAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08683426
Patent No. 5705367
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
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LENGTH: 306 amino acids
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MOLECULE TYPE: protein
US-08-683-426-4
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68; Gaps

Indels

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Floppy disk
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amino acid
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207 IVPPTLFAEQDFLNMYFK-----DIYKPIPPVYNLVL-AMLWRHPENIELDQ----- 252
                                  181 DV--MQYQDQDILNGLFKGGVCYANSRFNFMPTNYAFMANGFASRHTDPLYLDRTNTAMP 238
                                                                    -----DIKMLVKKW 287
                                                                                                                                                                                                                                      APPLICANT: GOLSCHLICH, EMIL C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
                                                                                            7.4%; Score 134; DB 2; Length 306; 25.0%; Pred. No. 1.4e-06;
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                                                                      253 VKVVHYCAAGAKPW------RFT---GEEENMDRE-
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CLASSIFICATION: 435
ATTORNEY, FAGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095B
TELECOMMUNICATION INFORMATION:
TELECHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,360
FILING DATE: 18-JUN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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411 Hackensack Avenue
                                                                                                                                                                                            Sequence 4, Application US/08878360 Patent No. 5945322
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 25.0%
Matches 59; Conservative
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                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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US-08-878-360-4
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TITLE OF INVENTION: SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSFERASE, A
TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE AND GENE ENCODING A
TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE
CORRESPONDENCES: 8
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 PQYKIGYCQQCPDKVTWPEAKLG-PKPPLYFNAGMFVYEPNLSTYHNL-----LETVK 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 VINYSKLRIWEFV-EYNKMIYLDGDIQVFDNIDHLFDLPNGQFY---AVMDCFCEKTWSHS 154
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                                      239 VAVSHYCGS-AKPWHRDCTVWGAERFTELAGSLTTVPEEWRGKLAVPPTKCMLQRW 293
253 VKVVHYCAAGAKPW------RFT---GEEENMDRE------DIKMLVKKW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68;
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                                                                                                                                                                                                                71; Indels
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7.4%; Score 134; DB 3;
Best Local Similarity 25.0%; Pred. No. 1.4e-06;
Matches 59; Conservative 38; Mismatches 71:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7188-017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                            Sequence 4, Application US/08478140B Patent No. 6127153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORREY/AGENT INFORMATION:
NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 718
TELECOMMUNICATION INFORMATION:
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71; Indels 68; Gaps
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Patent No. 6342382
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
OLIGOSACCHARIDES, AND GENES ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 VKVVHYCAAGAKPW------RFT---GEEENMDRE-------DIKMLVKKW 287
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-333-412-4
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ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
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COUNTRY: USA
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Search completed: July 2, 2002, 12:08:57 Job time: 174 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 2, 2002, 12:08:26; Search time 53.7 Seconds (without alignments) 692.918 Million cell updates/sec Run on:

US-09-810-506-2 1816 Perfect score:

1 MAPEINTKLTVPVHSATGGE.......FIEALSEAGALQYVKAPSAA 335 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

747574 seqs, 111073796 residues Searched:

Potal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Sequence encoded b	Sequence encoded b	Rice qlycogenin-li	Rice water stress-	Arabidopsis thalia	Arabidopsis thalia	Partial WSIP. Ory
	ΩI	AAG14525	AAG45747	AAG14526	AAG45748	AAR31580	AAR31581	AAW82560	AAE05241	AAG14527	AAG45749	AAB72462
	DB	21	21	21	21	14	14	13	22	21	21	22
	Query Match Length DB ID	344	344	333	333	330	328	328	328	279	279	117
r	Query	9.92	9.92	76.5	76.5	74.9	74.8	72.6	72.6	67.3	67.3	27.3
	Score	1390.5	1390.5	1389.5	1389.5	1360.5	1357.5	1319	1319	1222.5	1222.5	496
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ALIGNMENTS

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence. Arabidopsis thaliana protein fragment SEQ ID NO: 14420. AAG14525 standard; Protein; 344 AA. 99US-0121825. 99US-0123180. 99US-0123548. 99US-0125788. 99US-0126264. 99US-0126785. 99US-0127462. 99US-0128714. 99US-0129845. 99US-0130077. 99US-0130449. 25-FEB-2000; 2000EP-0301439 99US-0128234 (first entry) Arabidopsis thaliana 09-MAR-1999; 23-MAR-1999; 25-MAR-1999; 29-MAR-1999; EP1033405-A2 16-APR-1999; 19-APR-1999; 21-APR-1999; 17-OCT-2000 1999) 36-APR-1999; 06-SEP-2000 AAG14525; -APR-38-APR-AAG14525 ID AAG1 RESULT

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
Arabidopsis thaliana protein fragment SEQ ID NO: 14421.
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1;

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The nucleotide 1 is the first nucleotide following the Eco RI restriction site used in cloning the cDNA, reading from 5' to 3' on the cDNA insert, and nucleotide 1265 is the last nucleotide of the cDNA insert. The inventors claim a method of varying the level of D-galactose containing oligosaccharides of sucrose in plants in response to end-user requirements which involves combining the nucleic acid fragment of AAQ55603 and AAQ36504 with suitable regulatory sequences for expression and localization in plant tissues.
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                              dhlfdlpdgylyavmdcfcektwshtpgykirycgqcpdkvqwpkaelgeppalyfnagm 185
                                                                             FVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAMLWRHPENI
                                                                                                                        249 ELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLDYKN-VVIGDSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of galactinol synthase from zucchini and
                                                                                                                                                                                                                                                                                                                                                                                          Sequence encoded by zucchini leaf galactinol synthase cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                        Galactinol synthase; enzyme; raffinose saccharide; sucrose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     soybean – used to produce plants having altered levels of raffinose saccharide(s) and/or sucrose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pierce JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Becker-Manley MF, Kerr PS, Pearlstein RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Pages 59-61; 80pp; English.
                                                                                                                                                                                     308 KKQQTLQQFIEALSEAGALQYVKAPSAA 335
                                                                                                                                                                                                       (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                               AAR31580 standard; Protein; 330 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cucurbita pepo Burpee's hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91US-0735066.
                                                                                                                                                                                                                                                                                                                                                           06-JUN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1993-058793/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAQ36503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9302196-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                              126
129
                                                                                                                                                                                                                                                                              AAR31580
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The nucleotide 1 is the first nucleotide following the Eco RI restriction site used in cloning the cDNA, reading from 5' to 3' on the cDNA insert. and nucleotide 1265 is the last nucleotide of the cDNA insert. The inventors claim a method of varying the level of D-galactose containing oligosaccharides of sucrose in plants in response to end-user requirements which involves combining the nucleic acid fragment of AAO36503 and AAO36504 with suitable regulatory sequences for expression and localization in plant tissues.
196 STYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAMLWRHPENIELDQVKV 255
                                                                                                                               25 VHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLDYKNVVIGDSHKKQQTLQQ 315
                                                                                                                                                                                      NGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of galactinol synthase from zucchini and soybean - used to produce plants having altered levels of raffinose saccharide(s) and/or sucrose
                                                                                                                                                                                                                                                                                                                                                                                                                                               Galactinol synthase; enzyme; raffinose saccharide; sucrose.
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence encoded by soybean seed galactinol synthase cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pierce JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pearlstein RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Pages 61-63; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                 AAR31581 standard; Protein; 328
                                                                                                                                                                                                                                                : |||| : :: |||||
311 lvsvlseaevvnhitapsaa 330
                                                                                                                                                                                                                                316 FIEALSEAGALQYVKAPSAA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92WO-US06057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         910S-0735066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kerr PS,
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycine max Cultivar Wye.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-058793/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Becker-Manley MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAQ36504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schweiger BJ
                                                                                                                                                                                                                                                                                                                                                                                      06-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-1993.
                                                                                                                                                                                                                                                                                                                                                           AAR31581;
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4;

Gaps

74.8%; Score 1357.5; DB 14; Length 328; 74.3%; Pred. No. 2.7e-137; ive 29; Mismatches 45; Indels 13;

ilarity 74.3%; Pr Conservative 29;

Similarity

Query Match Best Local Simi Matches 251;

ij

1; Gaps

41; Indels

Query Match 74.9%; Score 1360.5; DB 3 Best Local Similarity 75.6%; Pred. No. 1.3e-137. Matches 242; Conservative 36; Mismatches 41.

DB 14; Length 330;

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This sequence represents a rice glycogenin-like water stress protein which is used in a method to isolate novel plant glycogenin proteins. Such proteins can be used to alter plant glycogenin and water stress protein expression. Manipulation of glycogenin expression can be used to alter starch biosynthesis and effects the number of starch granules in the endosperm of corn. Overexpression or reduction of expression of genes encoding glycogenin in corn, rice and wheat could be used to alter branch chain distribution of the starch produced by these plants.
                                                                                                                                                                                                                        LDGDIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLG 177
                                                                                                                                                                                                                                                  PKPPLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLV 237
                                                                                                                                                                                                                                                                                                                                                                  238 LAMIWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLD 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLPDVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIY 117
                                                                                                                                                                61 vlpdvpqdhrniltsqgcivreiepvyppenqtqfamayyvinysklriwefveyskmiy 120
                             57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycogenin; water stress protein; starch biosynthesis; corn; rice; wheat; plant; granules; branch chain; endosperm.
  1 MAPEINT-KLTVPVHSA--TGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant glycogenin and water stress proteins – used to alter plant glycogenin and water stress protein expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 YKNVVIGDSHKKQQTLQQFIEALSEAGALQYVKAPSAA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rice glycogenin-like water stress protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 33-34; 57pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW82560 standard; Protein; 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DUPO ) DU PONT DE NEMOURS & CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09850553-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lightner JE;
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                                                                                                               28
                                                                                                                                                                                                                           118
                                                                                                                                                                                                                                                                                                                                       178
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5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New glycogenin polynucleotides and polypeptides or water stress proteins, useful for encoding homologous glycogenins and water stress proteins from the same or other plant species -
                                                                                                                        PLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAM 240
                                                                                                                                                                                                                                                                                         LWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLDYKN 300
                                                                                                                                                                                                                                                                                                         121 DIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKP 180
                                                                                                      61 DVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDG 120
                                            1 MAPEINTKLTVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLP 60
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  water stress-induced protein; starch biosynthesis;
                                                                                                                                                                                                                                               The present sequence is water stress-induced protein from rice
              8
              Indels
 Pred. No. 3.8e-133;
1: Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                      301 VVIGDSHKKQQTLQQFIEALSEAGALQYVKAPSAA 335
                                                                                                                                                                                                                                                                                                                                                                       transgenic plant; plant breeding.
                 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE05241 standard; Protein; 328 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice water stress-induced protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 2; 33pp; English.
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71.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lightner JE, Everard JD;
                 238; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-432051/46.
 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rice; glycogenin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6255114-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycogen;
                                                                                                                                                                                                                                                                                            241
                   Matches
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is present at higher or lower levels than normal or in cell types or developmental stages in which it is not normally found. The nucleic acid fragments are also used as probes for genetically and physically mapping the genes that they are a part of, and as markers for traits linked to expression of a corn, rice and wheat glycogenin or water stress protein. The cDNRs of the invention are used in plant breeding to develop cell lines with desired starch phenotypes. The antibodies of glycogenin or water stress proteins are used to screen cDNA expression libraries to isolate full-length cDNA clones of interest.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                               DIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKP 180
                                                                                                                                                                                                                          PLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAM 240
                                                                                                                                                                                                                                                                                    LWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLDYKN 300
                                                                                                                                8; Gaps
                                                                                                                                               1 MAPEINTKLTVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLP 60
                                                                                                                                                         DB 22; Length 328;
                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 14422.
                                                                                                             72.6%; Score 1319; DB 22; 71.0%; Pred. No. 3.8e-133; ative 41; Mismatches 48;
                                                                                                                                                                                                                                                                                                                    301 VVIGDSHKKQQTLQQFIEALSEAGALQYVKAPSAA 335
                                                                                                                                                                                                                                                                                                                            AAG14527 standard; Protein; 279 AA.
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99US-0123180.
99US-012548.
99US-0125788.
99US-0126785.
99US-0126785.
99US-012834.
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                                                                                                                      Best Local Similarity 71.0%
Matches 238; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana.
                                                                                     328 AA;
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01-APR-1999;
06-APR-1999;
08-APR-1999;
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25-MAR-1999
                                                                                       Sequence
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990S-0139453.
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9905-0139462.
9905-0139463.
9905-0139763.
9905-0139817.
9905-0139817.
9905-0140353.
9905-0140823.
9905-0141842.
9905-0141842.
9905-0142390.
9905-0142390.
9905-0142390.
9905-0142390.
9905-0142390.
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99US-0139459.
99US-0139460.
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99US-0132486.
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99US-0134256.
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99US-0135629.
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99US-0132048
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16-APR-1999;
19-APR-1999;
23-APR-1999;
23-APR-1999;
28-APR-1999;
30-APR-1999;
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05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
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11-MAY-1999;
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14-MAY-1999;
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18-MAY-1999;
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24-MAY-1999;
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28-MAY-1999;
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22-OCT-1
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14-0CT-1
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18-0CT-1
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21-0CT-1
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The present invention relates to a method for determining the effect of a
                                                                                                                                                                                                                                                                                                                                                     test sample on UDP-glucose;glycoprotein glucosyltransferase (UGGT) a activity. The method comprises exposing an acceptor substrate for UGGT to a labelled donor in the presence of the test sample and UGGT. The method is useful for determining UGGT activity. In particular, the method is useful in glucosyltransferase assay and kinetics measurement for determining UGGT activity. UGGT is a soluble enzyme of the endoplasmic reticulum which catalyses the addition of a glucose residue onto a sparagine-linked oligosaccharides, which are present on incorrectly folded glycoproteins. The present sequence was used in a sequence homology comparison with rat UGGT (see AAF60732 and AAB72436) which was used in the method of the present invention.
                                                                                                                                                                                                                     Determining the effect of a test sample on UDP-glucose:glycoprotein glucosyltransferase (UGGT), useful for measuring UGGT activity, comprises exposing an acceptor substrate for UGGT to a labeled donor in the presence of UGGT -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 FVEYNKMIYLDGDIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 VTWPEAKLGPKPPLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKD 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycogenin; water stress protein; starch biosynthesis; corn; rice; wheat; plant; granules; branch chain; endosperm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Partial sequence, no start codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                      Thomas DY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.3%; Score 496; DB 22; 72.6%; Pred. No. 3.2e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corn glycogenin clone cc3.mn0001.f7 protein.
                                                                                                                                                                      Bergeron JJM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW82556 standard; Protein; 346 AA.
                                                                                                                                                                                                                                                                                                         Disclosure; Fig 10; 95pp; English.
                                                                                                                                       (CANA ) NAT RES COUNCIL CANADA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85; Conservative
                                                                                                                                                                      Dignard D,
                                                                                                                                                                                                 WPI; 2001-218358/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9850553-A1
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                                                                                                                                                                    Tessier DC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corn; glycogenin; water stress protein; glycogen; starch biosynthesis; transgenic plant; plant breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 EPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDLPNGQFY 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 AVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYHN 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 ------eit-------atgnnatl------fnsgvmviepsnctfrl 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 reayatilhsaseyvcgaitaaqsirqagstrdlvilvddtisdhhrkglesagwkvrii 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 KRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKEI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 LLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAMLWRHPENIELDQVK-----
                                                                                                                                                                                 Plant glycogenin and water stress proteins – used to alter plant glycogenin and water stress protein expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 fganppvlyvlhy--lgrkpwlcfrdydcnwnveilrefasdvaharwwkvhn 251
                                                                                                                                                                                                                                                                                                                                                                                                                               Corn glycogenin protein from cc3.mn0001.f7 clone.
                                                                         (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                              Claim la; Page 27-28; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE05237 standard; Protein; 346 AA.
              98WO-US09201.
                                           97US-0852615.
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                                                                                                                                   WPI; 1998-610384/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 346 AA;
                                                                                                                                                   N-PSDB; AAV69345
            06-MAY-1998;
                                           07-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6255114-B1
                                                                                                      Lightner JE;
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The present sequence is corn glycogenin protein from cc3.mn0001.f7 clone.

The present invention relates to plant glycogenin or water stress
proteins and their corresponding nucleic acid sequences. Glycogenin
is a self-glucosylating protein involved in the synthesis of glycogen
which plays a major role in starch blosynthesis. Over-expression
or reduction of glycogenin gene expression alters the branch chain
or stress proteins from the same or other plant species, or to create
transgenic plants in which an instant glycogenin or water stress protein
is present at higher or lower levels than normal or in cell types or
developmental stages in which it is not normally found. The nucleic acid
fevelopmental stages in which it is not normally found. The nucleic acid
fragments are also used as probes for genetically and physically mapping
the genes that they are a part of, and as markers for traits linked to
expression of a corn, rice and wheat glycogenin or water stress protein.
The chast of the invention are used in plant breeding to develop cell
innes with desired starch phenotypes. The antibodies of glycogenin or
water stress proteins are used to screen cDNA expression libraries to
solate full-length cDNA clones of interest.
                                                                                                                                                                                                                    New glycogenin polynucleotides and polypeptides or water stress proteins, useful for encoding homologous glycogenins and water stress proteins from the same or other plant species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 EPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDLPNGQFY 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 KRAYVIFLAGIGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKEI 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 fganppvlyvlhy--1grkpwlcfrdydcnwnveilrefasdvaharwwkvhn 251
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                                                                             (DUPO ) DU PONT DE NEMOURS & CO
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                                                                                                                                                                                                                                                                                                      Claim 5; Fig 1; 33pp; English.
98US-0073297.
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                                                                                                                   Lightner JE, Everard JD;
                                                                                                                                                         WPI; 2001-432051/46.
N-PSDB; AAD09245.
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06-MAY-1998;
                                     07-MAY-1997;
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AAG39868;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 n-vldsgdaanlallsrpelgvtftklhcwrlvgfekcvfldadtlvlgncdelferee- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 YHNLLETVKIVPPTLFA-----EQDFLNMYF-----KDIYKPIPPVYNLVLAMLWR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 QFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLST 197
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                                          Drosophila; developmental biology; cell signalling; insecticide;
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Matches 76; Conservative 54; Mismatches 94;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                   Arabidopsis thaliana protein fragment SEQ ID NO: 49390.
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990S-0132048
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